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TO: Karen A Lacourciere
Location: CM1/11D09
Art Unit: 1635
Tuesday, December 23, 2003
Case Serial Number: 09744679

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Lacourciere,

See attached results.

If you have any questions about this search feel free to contact me at any time.

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Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
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110595

RECEIVED

From: Lacourciere, Karen
Sent: Tuesday, December 16, 2003 5:38 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 09/744,679

DEC 17 2003

(STIC)

Please search SEQ ID NO:7 for 09/744,679

Thank-you!

Karen A. Lacourciere Ph.D.

CM1 11D09 GAU 1635
(703) 308-7523

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 12/23
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2003, 17:03:24 ; Search time 236 Seconds
(without alignments)
6268.187 Million cell updates/sec

Title: US-09-744-679-7

Perfect score: 548

Sequence: 1 cgcgaggtcgcttgacc.....ccatggtgtgttcacotg 548

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | ID | Description |
|------------|-------------|-------|--------|----|-----------------------------|
| 1 | 548 | 100.0 | 548 | 21 | AAZ50772 Human thrombin rec |
| 2 | 548 | 100.0 | 3472 | 20 | AAZ22191 Human thrombin rec |
| 3 | 548 | 100.0 | 3472 | 25 | ACA56730 Human signalling p |
| 4 | 548 | 100.0 | 3480 | 13 | AAQ28568 Human thrombin rec |
| 5 | 548 | 100.0 | 3480 | 21 | AAZ50771 Human thrombin rec |
| 6 | 548 | 100.0 | 3592 | 25 | ACC50141 Breast cancer asso |
| 7 | 548 | 100.0 | 3592 | 25 | ABZ42767 Human thrombin rec |
| 8 | 387 | 70.6 | 1278 | 24 | ABK70889 Human cDNA encodin |

| | | | | | | |
|----|-------|------|--------|----|----------|----------------------|
| 9 | 328.4 | 59.9 | 2910 | 18 | AAZ62461 | Thr-GPA1 fusion ge |
| 10 | 322.4 | 58.8 | 6546 | 21 | AAF21433 | Human low adenosin |
| 11 | 322.4 | 58.8 | 6546 | 21 | AAA35311 | Human adenosine re |
| 12 | 321 | 58.6 | 3182 | 21 | AAF21432 | Human low adenosin |
| 13 | 321 | 58.6 | 3182 | 21 | AAA35310 | Human adenosine re |
| 14 | 282.4 | 51.5 | 1764 | 15 | AAQ73590 | Fragment of the hu |
| 15 | 249 | 45.4 | 772 | 23 | AAZ68315 | DNA encoding novel |
| 16 | 240.8 | 43.9 | 1209 | 24 | ABK70887 | Human cDNA encodin |
| 17 | 184.2 | 33.6 | 1312 | 18 | AAZ93367 | Mouse thrombin rec |
| 18 | 148.2 | 27.0 | 6436 | 24 | ABL32681 | Human immune syste |
| 19 | 147 | 26.8 | 1116 | 24 | ABK70888 | Human cDNA encodin |
| 20 | 146.6 | 26.8 | 6436 | 24 | ABL32680 | Human immune syste |
| 21 | 146 | 26.6 | 572 | 21 | AAZ27044 | Human cell surface |
| 22 | 137.2 | 25.0 | 556 | 24 | ABQ23658 | Oligonucleotide fo |
| 23 | 137.2 | 25.0 | 556 | 24 | ABQ23659 | Oligonucleotide fo |
| 24 | 135.6 | 24.7 | 556 | 24 | ABQ23660 | Oligonucleotide fo |
| 25 | 135.6 | 24.7 | 556 | 24 | ABQ23661 | Oligonucleotide fo |
| 26 | 126.6 | 23.1 | 1300 | 19 | AAV33372 | PROLAC FLAG-conne |
| 27 | 125.4 | 22.9 | 1300 | 19 | AAV33371 | Fragment of thromb |
| 28 | 56 | 10.2 | 56 | 19 | AAV33375 | Fragment of thromb |
| 29 | 55 | 10.0 | 55 | 19 | AAV33376 | Micromonospora meg |
| 30 | 48.8 | 8.9 | 47981 | 22 | AAF30757 | Thrombin site-DR b |
| 31 | 46 | 8.4 | 54 | 19 | AAV33374 | Thrombin site-DR b |
| 32 | 44.6 | 8.1 | 192 | 18 | AAZ97178 | Human nervous syst |
| 33 | 44.4 | 8.1 | 12111 | 22 | ABA21422 | Mouse ischaemic co |
| 34 | 42 | 7.7 | 3272 | 24 | ABZ9475 | DNA encoding novel |
| 35 | 41.8 | 7.6 | 2259 | 23 | AAZ79424 | M. echinospora cal |
| 36 | 41.2 | 7.5 | 1362 | 25 | ABX56041 | WFS1 variant genom |
| 37 | 40.8 | 7.4 | 67212 | 21 | AAA08954 | Thrombin site-DR a |
| 38 | 40.6 | 7.4 | 189 | 18 | AAZ97177 | HSV-2 strain SB5 C |
| 39 | 40.6 | 7.4 | 2341 | 19 | AAV62155 | HSV-2 strain SB5 C |
| 40 | 40.6 | 7.4 | 2694 | 19 | AAV62145 | HSV-2 strain SB5 C |
| 41 | 40.6 | 7.4 | 117213 | 19 | AAV62176 | Human herpesvirus |
| 42 | 40.6 | 7.4 | 154746 | 24 | AAZ25519 | CNS disorder-relat |
| 43 | 40.4 | 7.4 | 327 | 23 | AAH88285 | Human cardiovascular |
| 44 | 40.2 | 7.3 | 32195 | 22 | AAZ36105 | Human DNA for a no |
| 45 | 40.2 | 7.3 | 32195 | 22 | AAZ31532 | |

ALIGNMENTS

RESULT 1
AAZ50772
ID AAZ50772 standard; cDNA; 548 BP.
XX
AC AAZ50772;
XX
AC
DT 31-MAY-2000 (first entry)
XX
Human thrombin receptor antisense cDNA.
XX
Human; thrombin receptor; Thr; PAR-1; protease activated receptor;
XX
antisense molecule; PAR antibody; cytostatic; therapeutic;
XX
metastatic tumour cell; placental implantation; invasive cell; ss.
XX
Homo sapiens.
XX
XX WO200008150-A1.
XX
PD 17-FEB-2000.
XX
PF 05-FEB-1999; 99WO-IL00079.
XX
PR 07-AUG-1998; 98IL-0125698.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Bar-Shavit R;
XX
DR WPI; 2000-205706/18.
XX
PT Treating metastatic tumor cells useful for treating disorders involving

Db 484 TCATCTCAGAGATGCTCCGGATATTGGACAGCTCCTGGCTGACACTCTTTGTCCCAT 543
QY 481 CTGTGTACACCGAGTGTGTGTAGTCAGCTCCACCTAAACATCATGGCCATCGTTGTGT 540
Db 544 CTGTGTACACCGAGTGTGTGTAGTCAGCTCCACCTAAACATCATGGCCATCGTTGTGT 603
QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 3
ACA56730
ID ACA56730 standard; cDNA; 3472 BP.
XX
AC ACA56730;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1328.
XX
DE Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
XX US6500938-B1
XX
XX 31-DEC-2002.
XX
XX 30-JAN-1998; 98US-0016434.
XX
XX 30-JAN-1998; 98US-0016434.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Au-Young J, Seilhamer JJ;
XX
XX WPI; 2003-352189/33.
XX
XX Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides -
XX
XX Claim 1; SEQ ID NO 1328; 65pp; English.
XX
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX forensics and pharmacogenomics. The microarray is also useful for
XX monitoring progression of diseases and for developing sophisticated
XX profiles for the effects of currently available therapeutic drugs. The
XX combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX and genomic fragments and in research and diagnostic applications. The
XX array can detect changes in expression in a large number of genes coding
XX for different signaling pathway populations which can be used to diagnose
XX various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX and Parkinson's disease. The present sequence represents a polynucleotide
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
XX
XX Sequence 3472 BP; 933 A; 817 C; 785 G; 937 T; 0 other;

Query Match 100.0%; Score 548; DB 25; Length 3472;
Best Local Similarity 100.0%; Pred. No. 1.3e-138; Indels 0; Gaps 0;
Matches 548; Conservative 0; Mismatches 0;

QY 1 CGCCGAGGGTTCGCTTGGACCCCTGATCTTACCCGTGGGACACCTCGCTGCTGCTGCGCG 60
Db 64 CGCCGAGGGTTCGCTTGGACCCCTGATCTTACCCGTGGGACACCTCGCTGCTGCTGCGCG 123
QY 61 AAGACCGGCTCCCGACCCCGCAGAGTTCAGGAGAGGGTGAAGCGGAGCCGCGAGGC 120
Db 124 AAGACCGGCTCCCGACCCCGCAGAGTTCAGGAGAGGGTGAAGCGGAGCCGCGAGGC 183
QY 121 GGGGACGCTCCCGGAGCAGCGCGCAGAGCCCGGACCAATGGGGCGCGGGGCTGC 180
Db 184 GGGGACGCTCCCGGAGCAGCGCGCGCAGAGCCCGGACCAATGGGGCGCGGGGCTGC 243
QY 181 TGCTGTGGCGCGCTGCTTCAGTCTGTGCGGCCCGCTGTTGTCTGCGCGCACCCGGGCCC 240
Db 244 TGCTGTGGCGCGCTGCTTCAGTCTGTGCGGCCCGCTGTTGTCTGCGCGCACCCGGGCCC 303
QY 241 GCAGGCCAGATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCTCAGGA 300
Db 304 GCAGGCCAGATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCTCAGGA 363
QY 301 ACCCAATGATAAATATGAACCATTTTGGGAGGATGAGGAGAGAAATGAAAGTGGGTTAA 360
Db 364 ACCCAATGATAAATATGAACCATTTTGGGAGGATGAGGAGAGAAATGAAAGTGGGTTAA 423
QY 361 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACCTTCTCGAT 420
Db 424 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACCTTCTCGAT 483
QY 421 TCATCTCAGAGATGCTCCCGGATATTTGACAGCTCTGCTGGCTGACACTCTTTGTCCTCAT 480
Db 484 TCATCTCAGAGATGCTCCCGGATATTTGACAGCTCTGCTGGCTGACACTCTTTGTCCTCAT 543
QY 481 CTGTGTACACCGGAGTGTGTTGTAGTCAGCTCCCACTAAACATCATGSCCATCTGTTGTGT 540
Db 544 CTGTGTACACCGGAGTGTGTTGTAGTCAGCTCCCACTAAACATCATGSCCATCTGTTGTGT 603
QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 4
AAQ28568
ID AAQ28568 standard; DNA; 3480 BP.
XX
AC AAQ28568;
XX
DT 25-MAR-2003 (updated)
DT 15-FEB-1993 (first entry)
XX
DE Human thrombin receptor gene.
XX
XX Diagnosis; cardiovascular disease; wound healing; restenosis;
KW thrombosis; unstable angina treatment; myocardial infarction;
KW thrombotic; thromboembolytic stroke; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 225..1502
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT 304..1502
FT /*tag= c
XX
XX WO9214750-A1.
XX
XX 03-SEP-1992.

```
XX PF 19-FEB-1992; 92WO-US01312.
XX PF
XX PR 19-FEB-1991; 91US-0657769.
XX PR 07-NOV-1991; 91US-0789184.
XX (CORT-) COR THERAPEUTICS INC.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Coughlin SR, Scarborough RM;
XX XX
XX DR WPI; 1992-316119/38.
XX DR P-PSDB; AAR27240.
XX XX
XX PT DNA encoding cell surface receptor for thrombin - useful for
XX PT determining thrombin in diagnosing e.g. cardiovascular diseases,
XX PT also to treat wound healing, restenosis etc.
XX XX
XX PS Disclosure; Fig 1; 81pp; English.
XX XX
XX CC The sequence is that of the gene coding for human thrombin receptor.
XX CC It can be used in the prep. of diagnostics to determine thrombin
XX CC levels in samples, and screening tools for candidate substances which
XX CC affect thrombin activity in vivo. Thrombosis may be diagnosed in a
XX CC mammal by measuring the presence, absence or amt. of the cleaved
XX CC activation peptide of the TR.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX XX
XX SQ Sequence 3480 BP; 947 A; 816 C; 786 G; 931 T; 0 other;

Query Match 100.0%; Score 548; DB 13; Length 3480;
Best Local Similarity 100.0%; Pred. No. 1.3e-138; Indels 0; Gaps 0;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCGAGGGTCCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCCGCG 60
Db 64 CGCCGAGGGTCCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCCGCG 123

Qy 61 AAGACCGGCTCCCGACCCGAGAGTCTAGAGAGAGGGTGAAGCGGAGAGCCCGAGGC 120
Db 124 AAGACCGGCTCCCGACCCGAGAGTCTAGAGAGAGGGTGAAGCGGAGAGCCCGAGGC 183

Qy 121 GGGGAGGCTCCCGAGAGCGCGCGAGAGCGCGGACCAATGGGCGCGGGGCTGC 180
Db 184 GGGGAGGCTCCCGAGAGCGCGCGAGAGCGCGGACCAATGGGCGCGGGGCTGC 243

Qy 181 TGCTGGTGGCGCGCTGCTTCAAGTCTGTGCGGCGCGCTGTGCTGCCGCAACCGGCGCC 240
Db 244 TGCTGGTGGCGCGCTGCTTCAAGTCTGTGCGGCGCGCTGTGCTGCCGCAACCGGCGCC 303

Qy 241 CGAGCCGAGATCAAAAGACCAATGCAATGCACTTACCTAGATCCCGGTCATTTCTTCAGGA 300
Db 304 CGAGCCGAGATCAAAAGACCAATGCAATGCACTTACCTAGATCCCGGTCATTTCTTCAGGA 363

Qy 301 ACCCCAAATGATAAATGAAACCAATTTGGAGAGATGAGAGAAAATGAAAGTGGGTTAA 360
Db 364 ACCCCAAATGATAAATGAAACCAATTTGGAGAGATGAGAGAAAATGAAAGTGGGTTAA 423

Qy 361 CTGAATACAGATGATGCTCCATCAATAAAGAGTCTCTTCAAAAACAACTTCTGCTAT 420
Db 424 CTGAATACAGATGATGCTCCATCAATAAAGAGTCTCTTCAAAAACAACTTCTGCTAT 483

Qy 421 TCATCTCAGAGATGCTCCGATATTTGACAGAGTCTTGGGCTGACACTCTTTGTCCTAT 480
Db 484 TCATCTCAGAGATGCTCCGATATTTGACAGAGTCTTGGGCTGACACTCTTTGTCCTAT 543

Qy 481 CTGTGTACACCGAGTGTGTTGATGACGCTCCCACTAAACATCATGCGCATCGTGTGT 540
Db 544 CTGTGTACACCGAGTGTGTTGATGACGCTCCCACTAAACATCATGCGCATCGTGTGT 603

Qy 541 TCATCTGT 548
Db 604 TCATCTGT 611
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RESULT 5

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AAZ50771
ID AAZ50771 standard; DNA; 3480 BP.
XX
XX AC AAZ50771;
XX DT 31-MAY-2000 (first entry)
XX DE Human thrombin receptor DNA.
XX KW Human; thrombin receptor; ThR; PAR-1; protease activated receptor;
XX KW antisense molecule; PAR antibody; cytostatic; therapeutic;
XX KW metastatic tumour cell; placental implantation; invasive cell; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 225..1502
XX FT /*tag= a
XX FT /product= "Thrombin receptor"
XX FT /transl_except= (pos:1500..1502, aa:Glx)
XX FT /note= "no stop codon given"
XX FT misc_binding 320..570
XX FT /*tag= b
XX FT /bound_moiety= "Thr RNA probe"
XX PN WO200008150-A1.
XX PD 17-FEB-2000.
XX PF 05-FEB-1999; 99WO-IL00079.
XX PR 07-AUG-1998; 98IL-0125698.
XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX PI Bar-Shavit R;
XX X WPI; 2000-205706/18.
XX DR P-PSDB; AAY45035.
XX PT Treating metastatic tumor cells useful for treating disorders involving
XX PT placenta implantation in a female comprises administration of an
XX PT antisense molecule complementary to an RNA sequence of a protease
XX PT activated receptor protein -
XX PS Example 2; Fig 1a; 46pp; English.
XX CC The patent discloses a method to treat metastatic tumour cells using
XX CC an antisense molecule comprising a polynucleotide complementary to an
XX CC RNA sequence of a protease activated receptor (PAR) protein, or an
XX CC antibody capable of binding to a PAR protein. The antisense molecules
XX CC with implantation of PAR protein are also used to treat disorders associated
XX CC with implantation of placenta. The present sequence is a DNA encoding
XX CC human thrombin receptor (ThR) (also known as PAR-1), which is a
XX CC G-coupled protein belonging to the PAR family. This sequence is used to
XX CC produce antisense molecules or antibodies against PAR protein for
XX CC therapeutic use.
XX SQ Sequence 3480 BP; 941 A; 817 C; 785 G; 937 T; 0 other;

Query Match 100.0%; Score 548; DB 21; Length 3480;
Best Local Similarity 100.0%; Pred. No. 1.3e-138; Indels 0; Gaps 0;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCGAGGGTCCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCCGCG 60
Db 64 CGCCGAGGGTCCGCTTGAGCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCCGCG 123

Qy 61 AAGACCGGCTCCCGACCCGAGAGTCTAGAGAGAGGGTGAAGCGGAGAGCCCGAGGC 120
```

Db 124 AAGACCGGCTCCCGAGCCCGCAGAAAGTCAGGAGAGAGGGTGAACGGGAGCAGCCCGAGGC 183
Qy 121 GGGCAGCGCTCCCGAGCAGCGCGCGCAGAGCCCGGAGCAATGGGCGCGGGGCTGC 180
Db 184 GGGCAGCGCTCCCGAGCAGCGCGCGCAGAGCCCGGAGCAATGGGCGCGGGGCTGC 243
Qy 181 TGCTGGTGGCGCGCTGCTTCAGTCTGTGCGGCGCGCTGTTGTCTGCGCGCACCCGGGCCC 240
Db 244 TGCTGGTGGCGCGCTGCTTCAGTCTGTGCGGCGCGCTGTTGTCTGCGCGCACCCGGGCCC 303
Qy 241 GCAGGCCAGAAATCAAAAGCAAAATGCGCACTTAGATCCCGGTCATCTTCTTCAGGA 300
Db 304 GCAGGCCAGAAATCAAAAGCAAAATGCGCACTTAGATCCCGGTCATCTTCTTCAGGA 363
Qy 301 ACCCAATGATAATATGAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAA 360
Db 364 ACCCAATGATAATATGAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAA 423
Qy 361 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAATCTTCTGCAT 420
Db 424 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAATCTTCTGCAT 483
Qy 421 TCATCTCAGAAAGTCCCGGATATTTGACGAGCTCTGCGTGCACACTCTTGTCCCAT 480
Db 484 TCATCTCAGAAAGTCCCGGATATTTGACGAGCTCTGCGTGCACACTCTTGTCCCAT 543
Qy 481 CTGTGTACACCGAGTGTGTTGTAGTCAGCCTCCCACTAAACATATGCCATCGTTGTGT 540
Db 544 CTGTGTACACCGAGTGTGTTGTAGTCAGCCTCCCACTAAACATATGCCATCGTTGTGT 603
Qy 541 TCATCCTG 548
Db 604 TCATCCTG 611
RESULT 6
ACC50141
ID ACC50141 standard; cDNA; 3592 BP.
XX
AC ACC50141;
DT 12-JUN-2003 (first entry)
DE Breast cancer associated cDNA sequence SEQ ID NO:129.
XX Human; breast cancer; cytostatic; gene therapy; gene; ss.
XX Homo sapiens.
OS
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US19669.
XX
PR 21-JUN-2001; 2001US-299887P.
PR 27-JUN-2001; 2001US-301572P.
PR 18-JUL-2001; 2001US-306501P.
PR 25-SEP-2001; 2001US-325002P.
PR 05-MAR-2002; 2002US-362585P.
PR 14-MAY-2002; 2002US-380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S, Mertens M;
PI Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE, Bast RC;
PI Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR P-PSDB; ABR47449.
XX
PT Breast cancer diagnosis or treatment by comparing the level of
PT expression of a marker in a patient sample with that in the control

PT non-breast cancer sample -
XX Claim 1; SEQ ID 129; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences
CC from the present invention have cytostatic activities and can be used in
CC gene therapy. The method is useful for diagnosing and treating breast
CC cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3592 BP; 950 A; 857 C; 837 G; 948 T; 0 other;
Query Match 100.0%; Score 548; DB 25; Length 3592;
Best Local Similarity 100.0%; Pred. No. 1.3e-138;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCGAGGGTGCCTTGGACCCCTGATCTTTACCGTGGGACCCCTGCTGCTGCGCGG 60
Db 184 CGCGAGGGTGCCTTGGACCCCTGATCTTTACCGTGGGACCCCTGCTGCTGCGCGG 243
Qy 61 AAGACCGGCTCCCGACCGCGAGAGTCAGGAGAGGGTGAAGCGGAGCAGCCCGAGGC 120
Db 244 AAGACCGGCTCCCGACCGCGAGAGTCAGGAGAGGGTGAAGCGGAGCAGCCCGAGGC 303
Qy 121 GGGGCGAGCTCCCGGAGCAGCGCCCGCAGAGCCCGGAGCAATGGGCGCGCGGCTGC 180
Db 304 GGGGCGAGCTCCCGGAGCAGCGCCCGCAGAGCCCGGAGCAATGGGCGCGCGGCTGC 363
Qy 181 TGCTGGTGGCGCGCTGCTTCAATCAATAAAGCAGTCTGTTGTGCGCGCGCTGTTGTG 240
Db 364 TGCTGGTGGCGCGCTGCTTCAATCAATAAAGCAGTCTGTTGTGCGCGCGCTGTTGTG 423
Qy 241 GCAGGCCAGAAATCAAAAGCAAAATGCGCACTTAGATCCCGGTCATCTTCTTCAGGA 300
Db 424 GCAGGCCAGAAATCAAAAGCAAAATGCGCACTTAGATCCCGGTCATCTTCTTCAGGA 483
Qy 301 ACCCAATGATAATATGAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAA 360
Db 484 ACCCAATGATAATATGAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAA 543
Qy 361 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAATCTTCTGCAT 420
Db 544 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAATCTTCTGCAT 603
Qy 421 TCATCTCAGAAAGTCCCGGATATTTGACGAGCTCTGCGTGCACACTCTTGTCCCAT 480
Db 604 TCATCTCAGAAAGTCCCGGATATTTGACGAGCTCTGCGTGCACACTCTTGTCCCAT 663
Qy 481 CTGTGTACACCGAGTGTGTTGTAGTCAGCCTCCCACTAAACATATGCCATCGTTGTGT 540
Db 664 CTGTGTACACCGAGTGTGTTGTAGTCAGCCTCCCACTAAACATATGCCATCGTTGTGT 723
Qy 541 TCATCCTG 548
Db 724 TCATCCTG 731
RESULT 7
ABZ42767
ID ABZ42767 standard; DNA; 3592 BP.
XX
AC ABZ42767;
XX
DT 04-MAR-2003 (first entry)

| | | | | | | |
|----|----|---|----|-----|--|-----|
| XX | DE | Human thrombin receptor nucleotide SEQ ID NO:323. | Db | 184 | CGCCGAGGGTGGCTTGGACCTGATCTTACCCGTGGGCACCCCTGGCTCTGCTGCTCCGCG | 243 |
| XX | KW | G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; | Qy | 61 | AAGACCGGCTCCCGACCCGAGAGTTCAGAGAGAGGGTCAAGCGAGAGCCGAGGC | 120 |
| XX | KW | G protein-coupled receptor modulator; antibody; immune-related disease; | Db | 244 | AAGACCGGCTCCCGACCCGAGAGTTCAGAGAGAGGGTCAAGCGAGAGCCGAGGC | 303 |
| XX | KW | growth-related disease; cell regeneration-related disease; AIDS; cancer; | Qy | 121 | GGGCGAGCTCCCGAGCGCCGCGAGAGCCGCGAGAGCCGCGCAATGGGGCGCGGGCTGC | 180 |
| XX | KW | immunological-related cell proliferative disease; autoimmune disease; | Db | 304 | GGGCGAGCTCCCGAGCGCCGCGAGAGCCGCGCAATGGGGCGCGGGCTGC | 363 |
| XX | KW | Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; | Qy | 181 | TGCTGGTGGCGCTGCTTCACTTCTGTGCGCGCGCTTGTGTCTCCCGCACCCGGGCC | 240 |
| XX | KW | osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; | Db | 364 | TGCTGGTGGCGCTGCTTCACTTCTGTGCGCGCGCTTGTGTCTCCCGCACCCGGGCC | 423 |
| XX | KW | graft versus host disease; Parkinson's disease; multiple sclerosis; pain; | Qy | 241 | GCAGCCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA | 300 |
| XX | KW | psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; | Db | 424 | GCAGCCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA | 483 |
| XX | KW | mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; | Qy | 301 | ACCCCAATGATAAATATGAAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGTTAA | 360 |
| XX | KW | hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; | Db | 484 | ACCCCAATGATAAATATGAAACCATTTTGGGAGGATGAGGAGAAAATGAAAGTGGTTAA | 543 |
| XX | OS | ulcer; gene; ds. | Qy | 361 | CTGAATACAGATTAGTCTCCATCAATAAAGAGCAGTCTCTTCAAAAACAATCTTCTGCAT | 420 |
| XX | OS | Homo sapiens. | Db | 544 | CTGAATACAGATTAGTCTCCATCAATAAAGAGCAGTCTCTTCAAAAACAATCTTCTGCAT | 603 |
| XX | PN | WO200261087-A2. | Qy | 421 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 480 |
| XX | PN | 08-AUG-2002. | Db | 604 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 663 |
| XX | PD | 19-DEC-2001; 2001WO-US50107. | Qy | 481 | CTGTGTACACCGAGTGTGTTGTAGTCAGCTCCCACTAAACATCATGCGCATCGTTGTGT | 540 |
| XX | PF | 19-DEC-2000; 2000US-257144P. | Db | 664 | CTGTGTACACCGAGTGTGTTGTAGTCAGCTCCCACTAAACATCATGCGCATCGTTGTGT | 723 |
| XX | PR | (LIFE-) LIFESPAN BIOSCIENCES INC. | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | PI | Burmer GC, Roush CL, Brown JP; | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | PI | WPI; 2003-046718/04. | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | PI | P-PSDB; ABP81919. | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | DR | New isolated antigenic peptides e.g., for G protein-coupled receptors | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | DR | (GPCR), useful for diagnosing and designing drugs for treating | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | PT | conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | PT | cancer or autoimmune diseases | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | PS | Disclosure; Fig 1; 523pp; English. | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | XX | | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | The present invention describes antigenic peptides (I) comprising: | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | acids. Also described: (1) an assay for the detection of a particular | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | and (2) an isolated antibody having high specificity and high affinity | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | or avidity for a particular GPCR. (I) can be used as GPCR modulators and | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | in gene therapy. The antigenic peptides for GPCRs are useful in detecting | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | an antibody against a particular GPCR, and in the production of specific | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | antibodies. The peptides and antibodies are also useful for detecting the | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | presence or absence of corresponding GPCRs. The antigenic peptides for | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | GPCRs and antibodies are useful for diagnosing and designing drugs for | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | treating immune-related diseases, growth-related diseases, cell | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | regeneration-related disease, immunological-related cell proliferative | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | atherosclerosis, bacterial, fungal, protozoan or viral infections, | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic acute | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | inflammation, allergies, Crohn's disease, diabetes, graft versus host | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | anxiety, depression, schizophrenia, dementia, mental retardation, memory | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | any other disorder in which GPCRs are involved. The antibodies may be | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | CC | GPCR proteins given in ABP81675 to ABP82018, which are used in the | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | CC | exemplification of the present invention. | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | XX | | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | SQ | Sequence 3592 BP; 950 A; 857 C; 837 G; 948 T; 0 other; | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | XX | Query Match 100.0%; Score 548; DB 25; Length 3592; | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | XX | Best Local Similarity 100.0%; Pred. No. 1.3e-138; | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |
| XX | XX | Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Db | 724 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 783 |
| XX | QY | 1 CGCCGAGGGTGGCTTGGACCTGATCTTACCCGTGGGCACCCCTGGCTCTGCTGCTCCGCG | Qy | 541 | TCATCTCAGAGATGCCCTCCGATATTTGACAGCTCTGCTGCTGACACTCTTTTGTCCCAT | 603 |

391 GCAGTCTCTTTCAAAACAACTTCTGATTCATCTCAGAAAGATGCTCCGGATATTGA 450
206 GCAGTCTCTTTCAAAACAACTTCTGATTCATCTCAGAAAGATGCTCCGGATATTGA 265
451 CCAGTCTCTGCTGACACTCTTTGTCCTCATCTGTCACACCGAGTGTTCAGTCAGCC 510
266 CCAGTCTCTGCTGACACTCTTTGTCCTCATCTGTCACACCGAGTGTTCAGTCAGCC 325
511 TCCCACTAAACATCATGCGCCATCGTTGTGTTTCATCCTG 548
326 TCCCACTAAACATCATGCGCCATCGTTGTGTTTCATCCTG 363

RESULT 10
AAF21433
ID AAF21433 standard; DNA; 6546 BP.
XX
AC AAF21433;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #3000.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PY (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1416-1418; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide

transmitters, defensins, growth factors, vasoactive peptides and
receptors, binding proteins and malignancy associated proteins. The
antisense oligonucleotides may be used in this way to treat disorders
including respiratory obstruction (especially pulmonary obstruction
and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
and/or surfactant hypoproduction which are associated with a disease or
condition selected from pulmonary vasoconstriction, inflammation,
allergies, asthma, impeded respiration, respiratory distress syndrome
(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
pulmonary transplantation rejection, pulmonary infections, bronchitis,
and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
fragments and antisense oligonucleotides used in the exemplification of
the present invention.

Sequence 6546 BP; 1603 A; 1691 C; 1500 G; 1751 T; 1 other;
Query Match 58.8%; Score 322.4; DB 21; Length 6546;
Best Local Similarity 99.7%; Pred. No. 3.2e-77;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 225 GCCGCGACCCCGCGCCGCGAGATCAAAAGCAAAATGCCACTTAGATCCCGG 284
DB 3362 GCAGCGACCCCGCGCCGCGAGATCAAAAGCAAAATGCCACTTAGATCCCGG 3421
QY 285 TCATTTCTTCTCAGGAACCCCAATGATAATATGAACCATTTTGGAGGATGAGGAGAA 344
DB 3422 TCATTTCTTCTCAGGAACCCCAATGATAATATGAACCATTTTGGAGGATGAGGAGAA 3481
QY 345 AATGAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAA 404
DB 3482 AATGAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAA 3541
QY 405 AAACAATCTCTGCTATTCATCTCAGAAAGTGCCTCCGATATTTGACCGCTCTGGCTG 464
DB 3542 AAACAATCTCTGCTATTCATCTCAGAAAGTGCCTCCGATATTTGACCGCTCTGGCTG 3601
QY 465 ACACCTCTTTTCCCATCTGTGTACACCGAGTGTGTAGTCAGCTCTCCACTAAACATC 524
DB 3602 ACACCTCTTTTCCCATCTGTGTACACCGAGTGTGTAGTCAGCTCTCCACTAAACATC 3661
QY 525 ATGGCCATCGTTGTGTTTCATCCTG 548
DB 3662 ATGGCCATCGTTGTGTTTCATCCTG 3685

RESULT 11
AAA35311
ID AAA35311 standard; DNA; 6546 BP.
XX
AC AAA35311;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:185.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PR 03-AUG-1999; 99WO-US17712.
XX

SQ Sequence 3182 BP; 895 A; 701 C; 684 G; 902 T; 0 other;

Query Match 58.6%; Score 321; DB 21; Length 3182;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 CGCACCCGGCCCGCAGGCGCAGATCAAAAGCAGCAAAATGCCACCTTAGATCCCCGGTCA 287
 DB 1 CGCACCCGGCCCGCAGGCGCAGATCAAAAGCAGCAAAATGCCACCTTAGATCCCCGGTCA 60

QY 288 TTTCTTCTCAGGAACCCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAAT 347
 DB 61 TTTCTTCTCAGGAACCCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAAT 120

QY 348 GAAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGACAGTCTCTTCAAAAA 407
 DB 121 GAAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGACAGTCTCTTCAAAAA 180

QY 408 CAATCTTCCTGCATTCATCTCAGAAAGATGCTCCGGATATTTGACCACTCTCTGGCTGACA 467
 DB 181 CAATCTTCCTGCATTCATCTCAGAAAGATGCTCCGGATATTTGACCACTCTCTGGCTGACA 240

QY 468 CTCTTTGTCCCATCTGTGTACACCGGAGTGTCTTGTAGTCAGCCTCCCACTAAACATCATG 527
 DB 241 CTCTTTGTCCCATCTGTGTACACCGGAGTGTCTTGTAGTCAGCCTCCCACTAAACATCATG 300

QY 528 GCCATCGTTGTGTTTCATCTCTG 548
 DB 301 GCCATCGTTGTGTTTCATCTCTG 321

RESULT 13
 AAA35310
 ID AAA35310 standard; DNA; 3182 BP.
 XX
 AC AAA35310;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:184.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antilasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 1330-1331; 1343pp; English.
 XX

CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antilasthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX
 SQ Sequence 3182 BP; 895 A; 701 C; 684 G; 902 T; 0 other;

Query Match 58.6%; Score 321; DB 21; Length 3182;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 CGCACCCGGCCCGCAGGCGCAGATCAAAAGCAGCAAAATGCCACCTTAGATCCCCGGTCA 287
 DB 1 CGCACCCGGCCCGCAGGCGCAGATCAAAAGCAGCAAAATGCCACCTTAGATCCCCGGTCA 60

QY 288 TTTCTTCTCAGGAACCCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAAT 347
 DB 61 TTTCTTCTCAGGAACCCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAAT 120

QY 348 GAAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGACAGTCTCTTCAAAAA 407
 DB 121 GAAAGTGGGTAACTGAATACAGATTAGTCTCCATCAATAAAGACAGTCTCTTCAAAAA 180

QY 408 CAATCTTCCTGCATTCATCTCAGAAAGATGCTCCGGATATTTGACCACTCTCTGGCTGACA 467
 DB 181 CAATCTTCCTGCATTCATCTCAGAAAGATGCTCCGGATATTTGACCACTCTCTGGCTGACA 240

QY 468 CTCTTTGTCCCATCTGTGTACACCGGAGTGTCTTGTAGTCAGCCTCCCACTAAACATCATG 527
 DB 241 CTCTTTGTCCCATCTGTGTACACCGGAGTGTCTTGTAGTCAGCCTCCCACTAAACATCATG 300

QY 528 GCCATCGTTGTGTTTCATCTCTG 548
 DB 301 GCCATCGTTGTGTTTCATCTCTG 321

RESULT 14
 AAQ73590
 ID AAQ73590 standard; DNA; 1764 BP.
 XX
 AC AAQ73590;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-JUN-1995 (first entry)
 XX
 DE Fragment of the human thrombin receptor gene.
 XX
 KW TR; expression; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers

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FT CDS 376..1653
XX /*tag= a
XX
XX PN WO9421789-A1.
XX
XX PD 29-SEP-1994.
XX
XX PF 28-FEB-1994; 94WO-US02388.
XX
XX PR 25-MAR-1993; 93US-0038662.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Betlach MC, Turner GJ;
XX
XX DR WPI; 1994-317010/39.
XX
XX DR P-PSDB; AAR60698.
XX
XX PT Expression of heterologous proteins in halo-bacteria - using
XX regulatory and stop sequences from halo-bacteria, pref. the
XX bacterio-rhodopsin gene.
XX
XX PS Disclosure; Fig 14; 118pp; English.
XX
XX CC The sequence is that of the human thrombin receptor gene fragment.
XX The gene is used to exemplify a new expression vector for producing
XX heterologous polypeptides in a halobacterial host.
XX See also AAQ73586-92.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 1764 BP; 382 A; 492 C; 421 G; 469 T; 0 other;
XX
XX Query Match 51.5%; Score 282.4; DB 15; Length 1764;
XX Best Local Similarity 99.6%; Pred. No. 1.4e-66;
XX Matches 283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 265 ATGCCACCTAGATCCCGGTGATTTCTTCAGGAACCCCAATGATAAATATGAACCAT 324
XX Db
XX QY 461 ACGCCACCTTAGATCCCGGTGATTTCTTCAGGAACCCCAATGATAAATATGAACCAT 520
XX Db
XX QY 325 TTTCGGAGATCAGGAGAAATGAAGTGGTAACTGAATACAGATTAGTCTCATCA 384
XX Db
XX QY 521 TTTCGGAGATCAGGAGAAATGAAGTGGTAACTGAATACAGATTAGTCTCATCA 580
XX Db
XX QY 385 ATAAAAGCAGTCTCTTCAAAAACAACTTCCTGCATTCATCTCAGAAAGATGCTCCGGAT 444
XX Db
XX QY 581 ATAAAAGCAGTCTCTTCAAAAACAACTTCCTGCATTCATCTCAGAAAGATGCTCCGGAT 640
XX
XX QY 445 ATTTGACAGCTCTGGCTGACACTTTTGTCCCATCTGTGTACACCGAGTGTGTGTAG 504
XX Db
XX QY 641 ATTTGACAGCTCTGGCTGACACTTTTGTCCCATCTGTGTACACCGAGTGTGTGTAG 700
XX
XX QY 505 TCAGCTCCCACTAAACATCATGGCCATCGTGTGTTCATCTGT 548
XX Db
XX QY 701 TCAGCTCCCACTAAACATCATGGCCATCGTGTGTTCATCTGT 744
XX
XX RESULT 15
XX AAS68315
XX ID AAS68315 standard; cDNA; 772 BP.
XX
XX AC AAS68315;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE DNA encoding novel human diagnostic protein #4119.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
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XX 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Drmanac RT, Liu C, Tang YT;
XX
XX DR WPI; 2001-639362/73.
XX
XX DR P-PSDB; ABG04128.
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX PS Claim 1; SEQ ID No 4119; 103pp; English.
XX
XX CC The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX
XX CC Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 772 BP; 194 A; 191 C; 223 G; 164 T; 0 other;
XX
XX Query Match 45.4%; Score 249; DB 23; Length 772;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-57;
XX Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 CGCCGAGGTCGCTTGGACCTGATCTTACCGTGGGCACCCCTGCGCTCTGCTGCGCG 60
XX Db
XX QY 96 CGCCGAGGTCGCTTGGACCTGATCTTACCGTGGGCACCCCTGCGCTCTGCTGCGCG 155
XX
XX QY 61 AAGACCGGCTCCCGACCCGAGAGTCAAGGAGAGGGTGAAGCGGAGAGCCGAGCC 120
XX Db
XX QY 156 AAGACCGGCTCCCGACCCGAGAGTCAAGGAGAGGGTGAAGCGGAGAGCCGAGCC 215
XX
XX QY 121 GGGGAGCGCTCCCGGAGAGCGCCGCGAGAGCCCGGGGCAATGGGGCGCGGCGTGC 180
XX Db
XX QY 216 GGGGAGCGCTCCCGGAGAGCGCCGCGAGAGCCCGGGGCAATGGGGCGCGGCGTGC 275
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XX QY 181 TGCTGTGCGCGCTGCTTACGTCGTGTGCGGCGCGCTGTGTGTGTCGCCGAGCC 240
XX Db
XX QY 276 TGCTGTGCGCGCTGCTTACGTCGTGTGCGGCGCGCTGTGTGTGTCGCCGAGCC 335
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XX Db
XX QY 336 GCAGGCCAG 344
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XX Search completed: December 20, 2003, 22:16:53
XX Job time : 238 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2003, 20:04:31 ; Search time 2381 Seconds
(without alignments)
9415.571 Million cell updates/sec

Title: US-09-744-679-7

Perfect score: 548

Sequence: 1 cgccgaggtgccttgacc.....ccatgtgtgttcctcgtg 548

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

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33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rod.*

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37: em_hg_vrt.*

38: em_sy.*

39: em_hngo_hum.*

40: em_hngo_mus.*

41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|-----------|--------------------|
| 1 | 548 | 100.0 | 3448 | 9 | BC051909 | BC051909 Homo sapi |
| 2 | 548 | 100.0 | 3472 | 6 | AR270765 | AR270765 Sequence |
| 3 | 548 | 100.0 | 3472 | 9 | HUMTHR | M62424 Human throm |
| 4 | 548 | 100.0 | 3479 | 9 | BC002464 | BC002464 Homo sapi |
| 5 | 548 | 100.0 | 3480 | 6 | AR025392 | AR025392 Sequence |
| 6 | 548 | 100.0 | 3480 | 6 | AR027730 | AR027730 Sequence |
| 7 | 548 | 100.0 | 3480 | 6 | AR065265 | AR065265 Sequence |
| 8 | 548 | 100.0 | 3480 | 6 | AR137610 | AR137610 Sequence |
| 9 | 548 | 100.0 | 3480 | 6 | I74660 | I74660 Sequence 21 |
| 10 | 548 | 100.0 | 3592 | 6 | AX549038 | AX549038 Sequence |
| 11 | 441.6 | 80.6 | 3764 | 9 | AF028727 | AF028727 Papio ham |
| 12 | 387 | 70.6 | 1278 | 6 | BD107008 | BD107008 Cell grow |
| 13 | 387 | 70.6 | 1278 | 9 | BT007279 | BT007279 Homo sapi |
| 14 | 306.2 | 55.9 | 70679 | 2 | AC026151 | AC026151 Homo sapi |
| 15 | 302 | 55.1 | 24771 | 9 | AF391809 | AF391809 Homo sapi |
| 16 | 302 | 55.1 | 110965 | 2 | AC020927 | AC020927 Homo sapi |
| 17 | 302 | 55.1 | 143335 | 9 | AC025188 | AC025188 Homo sapi |
| 18 | 282.4 | 51.5 | 1764 | 6 | I49726 | I49726 Sequence 12 |
| 19 | 249 | 45.4 | 88881 | 2 | AC008933 | AC008933 Homo sapi |
| 20 | 246 | 44.9 | 2895 | 9 | HSU63331 | U63331 Human throm |
| 21 | 240.8 | 43.9 | 1209 | 6 | BD107006 | BD107006 Cell grow |
| 22 | 229 | 41.8 | 2878 | 9 | AF054633 | AF054633 Homo sapi |
| 23 | 200.2 | 36.5 | 157274 | 2 | AC143142 | AC143142 Macaca mu |
| 24 | 188.2 | 34.3 | 2855 | 10 | CLTHRECC | X61958 C.longicaud |
| 25 | 184.2 | 33.6 | 1312 | 10 | MUSTHRRCT | L03529 Mus musculu |
| 26 | 183 | 33.4 | 3313 | 10 | BC031516 | BC031516 Mus muscu |
| 27 | 171.2 | 31.2 | 3418 | 10 | RATRGPC | M81642 Rat G-prote |
| 28 | 161 | 29.4 | 5457 | 9 | HSU36755 | U36755 Human throm |
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| 30 | 147 | 26.8 | 1116 | 6 | BD107007 | BD107007 Cell grow |
| 31 | 146.6 | 26.8 | 6436 | 6 | AX345582 | AX345582 Sequence |
| 32 | 137.6 | 25.1 | 182064 | 2 | AC130634 | AC130634 Rattus no |
| 33 | 133 | 24.3 | 5620 | 10 | MMTHREC02 | U36757 Mus musculu |
| 34 | 133 | 24.3 | 199227 | 2 | AC110876 | AC110876 Mus muscu |
| 35 | 133 | 24.3 | 235097 | 2 | AC110877 | AC110877 Mus muscu |
| 36 | 130.4 | 23.8 | 1164 | 10 | CLU34047 | U34047 Cricetulus |
| 37 | 125.4 | 22.9 | 1300 | 6 | AR212890 | AR212890 Sequence |
| 38 | 125.4 | 22.9 | 1300 | 6 | AR212893 | AR212893 Sequence |
| 39 | 123.8 | 22.6 | 1300 | 6 | AR212894 | AR212894 Sequence |
| 40 | 123.6 | 22.6 | 1298 | 6 | AR212891 | AR212891 Sequence |
| 41 | 56 | 10.2 | 56 | 6 | AR212873 | AR212873 Sequence |
| 42 | 55 | 10.0 | 55 | 6 | AR212874 | AR212874 Sequence |
| 43 | 53 | 9.7 | 275 | 10 | MMCF2R01 | U55075 Mus musculu |
| 44 | 53 | 9.7 | 4605 | 10 | MMTHREC01 | U36756 Mus musculu |
| 45 | 52.6 | 9.6 | 1680 | 5 | XLU09632 | U09632 Xenopus lae |

ALIGNMENTS

| | | | | | |
|------------|--|--|------|--------|-----------------|
| RESULT 1 | BC051909 | 3448 bp | mRNA | linear | PRI 05-MAY-2003 |
| LOCUS | BC051909 | Homo sapiens coagulation factor II (thrombin) receptor, mRNA (cdna clone MGC:60377 IMAGE:6172703), complete cds. | | | |
| DEFINITION | BC051909 | | | | |
| ACCESSION | BC051909 | | | | |
| VERSION | BC051909.1 | GI:30354671 | | | |
| KEYWORDS | MGC. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | 1 | (bases 1 to 3448) | | | |
| AUTHORS | Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., | | | | |

| | |
|-----------|---|
| TITLE | human and mouse cDNA sequences |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) |
| MEDLINE | 22388257 |
| PUBMED | 12477932 |
| REFERENCE | 2 (bases 1 to 3448) |
| AUTHORS | Strausberg,R. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov |
| COMMENT | Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M. |

Clone distribution: MGC clone distribution information can be found through the I.N.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 110 Row: m Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6031164.
 Location/Qualifiers
 1..3448
 source

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YVFSGSDMOFGSELRCFVFAAFYCNMYASITLLMTVTSIDRF LAVYVPMQSLSWRTLGR
ASFTCLAIWALAIAGVYVPLLKEQTTQVGLNITTTCHDVLNETLLGGYIAYYFSAFSA
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```

[illegible]

| | | | | | | |
|-----------------------|--|------------------------------|-----------|--------------|----|-----------------|
| RESULT 2 | | | | | | PAT 10-APR-2003 |
| AR270765 | | | | | | |
| LOCUS | | | | | | |
| DEFINITION | AR270765 | 3472 bp | DNA | linear | | |
| ACCESSION | Sequence | 1328 from patent US 6500938. | | | | |
| VERSION | AR270765 | .1 GI:29701999 | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unknown. | | | | | |
| REFERENCE | Unclassified. | | | | | |
| AUTHORS | 1 (bases 1 to 3472) | | | | | |
| TITLE | Au-Young, J. and Seilhamer, J.J. | | | | | |
| JOURNAL | Composition for the detection of signaling pathway gene expression | | | | | |
| FEATURES | Patent: US 6500938-A 1328 31-DEC-2002; | | | | | |
| | Location/Qualifiers | | | | | |
| | i..3472 | | | | | |
| | /organism="unknown" | | | | | |
| BASE COUNT | 933 a | 817 c | 785 g | 937 t | | |
| ORIGIN | | | | | | |
| Query Match | | | | | | |
| Best Local Similarity | 100.0%; | Score 548; | DB 6; | Length 3472; | | |
| Matches 548: | Conservative | 0; Mismatches | 0; Indels | 0; Gaps | 0; | |

QY 1 CGCCGAGGCTCGCTTGGACCTGATCTTACCCCTGGSCACCCCTCGCTCTGCCTGCGCG 60
Db 64 CGCCGAGGCTCGCTTGGACCTGATCTTACCCCTGGSCACCCCTCGCTCTGCCTGCGCG 123
QY 61 AAGACCGGCTCCCGAGCCGAGAGCTCAGAGAGAGGCTGAAGCGAGCAGCCGAGGC 120
Db 124 AAGACCGGCTCCCGAGCCGAGAGCTCAGAGAGAGGCTGAAGCGAGCAGCCGAGGC 183
QY 121 GGGGCGAGCTCCCGAGCAGCGCGCGAGAGCCGAGCAATGGGGCGCGCGGCTGC 180
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Db 424 CTGAATACAGATTAGTCTCAATCAATAAAGAGAGTCTCTTCAAAACAACTTCTGCAT 483
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QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 3
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LOCUS M62424.1 GI:339676
DEFINITION Human thrombin receptor mRNA, complete cds.
ACCESSION M62424.1
VERSION 1
KEYWORDS thrombin receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Vu, T.K., Hung, D.T., Wheaton, V.I. and Coughlin, S.R.
TITLE Molecular cloning of a functional thrombin receptor reveals a novel
proteolytic mechanism of receptor activation
JOURNAL Cell 64 (6), 1057-1068 (1991)
MEDLINE 91168254
PUBMED 1672265
COMMENT Original source text: Human DNA.
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LRNPNDKYEPFDEKESGLTEYRLVLSINKSPLOKQLPAFISEDASGLTSSWLT
CDS

BASE COUNT 933 a 817 c 785 g 937 t
ORIGIN
Query Match 100.0%; Score 548; DB 9; Length 3472;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCGAGGCTCGCTTGGACCTGATCTTACCCCTGGSCACCCCTCGCTCTGCCTGCGCG 60
Db 64 CGCCGAGGCTCGCTTGGACCTGATCTTACCCCTGGSCACCCCTCGCTCTGCCTGCGCG 123
QY 61 AAGACCGGCTCCCGAGCAGCGCGCGAGAGCTCAGAGAGAGGCTGAAGCGAGCAGCCGAGGC 120
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QY 121 GGGGCGAGCTCCCGAGCAGCGCGCGAGAGCCGAGCAATGGGGCGCGCGGCTGC 180
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QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 4
BC002464 3479 bp mRNA linear PRI 12-JUL-2001
LOCUS Homo sapiens, coagulation factor II (thrombin) receptor, clone
DEFINITION MGC:1197 IMAGE:3343051, mRNA, complete cds.
ACCESSION BC002464
VERSION BC002464.1 GI:12803296
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3479)
Direct Submission
TITLE Strausberg, R.
SUBMITTED (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, W., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.B., Touchman, J.W., Teague, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 5 Row: P Column: 3
This clone was selected for full length sequencing because it
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BASE COUNT 969 a 792 c 778 g 940 t
ORIGIN
Query Match 100.0%; Score 548; DB 9; Length 3479;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGAGGGTTCGCTTGACCCCTGATCTTACCCGTGGGCACCCCTGCGCTCTGCGCTGCGCGG 60
DB 29 CGCCGAGGGTTCGCTTGACCCCTGATCTTACCCGTGGGCACCCCTGCGCTCTGCGCTGCGCGG 88
QY 61 AAGACCGGCTCCCGAGCAGCCGAG 120
DB 89 AAGACCGGCTCCCGAGCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
QY 121 GGGGACGCTCCCGAGCAGCCGAG 180
DB 149 GGGGACGCTCCCGAGCAGCCGAG 208
QY 181 TGCTGTGGCGGCTGCTTCAGTCTGTGCGCGCGCGCTGTGTGTCTGCGCGCGCGCGCGCGCG 240
DB 209 TGCTGTGGCGGCTGCTTCAGTCTGTGCGCGCGCGCTGTGTGTCTGCGCGCGCGCGCGCGCG 268
QY 241 GCAGGCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA 300

269 GCAGGCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA 328
301 ACCCAATGATTAATATGAAACCAATTTTGGAGAGATGAGGAGAAAAATGAAAGTGGGTAA 360
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RESULT 5
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DEFINITION Sequence 219 from patent US 5798248
ACCESSION AR025392
VERSION AR025392.1 GI:3978020
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3480)
AUTHORS Coughlin, S.R. and Scarborough, R.M.
TITLE Recombinant mutant thrombin receptor and related pharmaceuticals
JOURNAL Patent: US 5798248-A 219 25-AUG-1998;
FEATURES
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Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGAGGGTTCGCTTGACCCCTGATCTTACCCGTGGGCACCCCTGCGCTCTGCGCTGCGCGG 60
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QY 61 AAGACCGGCTCCCGAGCAGCCGAG 120
DB 124 AAGACCGGCTCCCGAGCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
QY 121 GGGGACGCTCCCGAGCAGCCGAG 180
DB 184 GGGGACGCTCCCGAGCAGCCGAG 243
QY 181 TGCTGTGGCGGCTGCTTCAGTCTGTGCGCGCGCGCTGTGTGTCTGCGCGCGCGCGCGCGCG 240
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QY 241 GCAGGCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA 300
DB 304 GCAGGCGAGATCAAAAGCAAAATGCCACCTTAGATCCCGGTCATTTCTTCTCAGGA 363
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QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 6
AR027730
LOCUS AR027730 3480 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 219 from patent US 5856448.
ACCESSION AR027730
VERSION AR027730.1 GI:5938550
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3480)
AUTHORS Coughlin,S.R.
TITLE Antibodies specifically reactive with thrombin receptor and its components
JOURNAL Patent: US 5856448-A 219 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..3480
BASE COUNT 941 a 817 c 785 g 937 t
ORIGIN

Query Match 100.0%; Score 548; DB 6; Length 3480;
Best Local Similarity 100.0%; Pred. No. 1.le-111;
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QY 1 CGCCGAGGGTCCGCTTGGACCCCTCATCTTACCCCTGGGACCCCTGCGCTCTGCTGCGCG 60
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Db 124 AAGACCGGTCCCGACCCCGCAGAAAGTCAGGAGAGGGTGAAGCGAGCAGCCGAGGC 183
QY 121 GGGGAGCCTCCCGAGCAGCGCCGCGAGCGGCAATGGGGCCCGCGCGCTGC 180
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RESULT 7
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LOCUS AR065265 3480 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 219 from patent US 5849507.
ACCESSION AR065265
VERSION AR065265.1 GI:5995481
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3480)
AUTHORS Coughlin,S.R.
TITLE Methods to diagnose thrombosis by measuring activation peptide
JOURNAL Patent: US 5849507-A 219 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..3480
BASE COUNT 941 a 817 c 785 g 937 t
ORIGIN

Query Match 100.0%; Score 548; DB 6; Length 3480;
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Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGACCGGTCCCGACCCCGCAGAAAGTCAGGAGAGGGTGAAGCGAGCAGCCGAGGC 120
Db 124 AAGACCGGTCCCGACCCCGCAGAAAGTCAGGAGAGGGTGAAGCGAGCAGCCGAGGC 183
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Db 184 GGGGAGCCTCCCGAGCAGCGCCGCGAGCGGCAATGGGGCCCGCGCGCTGC 243
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QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

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| JOURNAL | Patent: WO 02061087-A 323 08-AUG-2002; |
| REFERENCE | Lifespan Biosciences, Inc. (US) |
| FEATURES | Location/Qualifiers |
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| | /db_xref="taxon:9606" |
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| QY | 61 AAGACCGGCTCCCGACCCCGCAGAGTCAAGAGAGGGTGAAGCGAGCGCCGAGGC 120 |
| Db | 244 AAGACCGGCTCCCGACCCCGCAGAGTCAAGAGAGGGTGAAGCGAGCGCCGAGGC 303 |
| QY | 121 GGGCGAGCTCCCGAGCAGCGCGCGCAGAGCCCGGCAATGGGCGCGGGGCTGC 180 |
| Db | 304 GGGCGAGCTCCCGAGCAGCGCGCGCAGAGCCCGGCAATGGGCGCGGGGCTGC 363 |
| QY | 181 TGTGTGGCGCGCTGCTTCACTGTGTGGCGCGCGCTGTTGTCTGCGCGCGCC 240 |
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| QY | 241 GCAGGCGAGAAATCAAAAGCAACAAATGCCACCTTAGATCCCGGTCAATTTCTCAGGA 300 |
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| QY | 421 TCATCTCAGAAAGTGTCTCGGATATTTGACAGCTCTGCTGACACTTTTGTCCCAT 480 |
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| QY | 481 CTGTGTACACCGAGTGTGTGTAGTCAGCTTCCCACTAAACATCATGGCCATCGTTGTGT 540 |
| Db | 664 CTGTGTACACCGAGTGTGTGTAGTCAGCTTCCCACTAAACATCATGGCCATCGTTGTGT 723 |
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| Db | 724 TCATCTGT 731 |
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| AF028727 | |
| LOCUS | Papio hamadryas thrombin receptor (bthr12) mRNA linear PRI 20-NOV-2000 |
| DEFINITION | AF028727 |
| ACCESSION | AF028727 |
| VERSION | AF028727.1 GI:2605876 |
| KEYWORDS | |
| SOURCE | Papio hamadryas (hamadryas baboon) |
| ORGANISM | Papio hamadryas |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Papio. |
| AUTHORS | 1 (bases 1 to 3764) |
| TITLE | Hayzer, D.J., Shoji, M. and Hanson, S.R. cDNAs encoding the baboon thrombin receptor indicate a primate transcription start site upstream of putative sites reported for the human gene |
| JOURNAL | Thromb. Res. 98 (2), 195-201 (2000) |
| MEDLINE | 20180190 |
| PUBMED | 10713321 |
| REFERENCE | 2 (bases 1 to 3764) |
| AUTHORS | Shoji, M., Hayzer, D.J. and Hanson, S.R. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (07-OCT-1997) Hematologic Diseases Division, Building 1, CDC/NCID/DHA, Rm. 1310, Mail Stop D-02, 1600 Clifton Road, Atlanta, GA 30333, USA |
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| Query Match | 80.6%; Score 441 6; DB 9; Length 3764; |
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| Matches | 503; Conservative 0; Mismatches 34; Indels 11; Gaps 3; |
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| Db | 382 CGCGGAGGGTGGCTTGAACCTGATCTTACCCGTGGGACCCCTCGCTCTGCTGCGCG 432 |
| QY | 61 AAGACCGGCTCCCGAGCAGCGCGCGCAGAGTCAAGAGAGGGTGAAGCGAGCGCCGAGGC 120 |
| Db | 433 AAGACCGGCTCCCGAGCAGCGCGCGCAGAGTCAAGAGAGGGTGAAGCGAGCGCCGAGGC 491 |
| QY | 121 GGGCGAGCTCCCGAGCAGCGCGCGCAGAGCGCGGCAATGGGCGCGGGGCTGC 180 |
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| QY | 541 TCATCTGT 548 |


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----- Project Information
Center project name: L8625
Center clone name: 329_A_20
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* NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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| * | 1869 | 2679: | contig of 811 | bp in length |
| * | 2680 | 2779: | gap of 100 | bp |
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| * | 3584 | 3683: | gap of 100 | bp |
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| * | 6341 | 6440: | gap of 100 | bp |
| * | 6441 | 7270: | contig of 830 | bp in length |
| * | 7271 | 7370: | gap of 100 | bp |
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| * | 12889 | 13702: contig of 814 bp in length |
| * | 13803 | 13802: gap of 100 bp |
| * | 14635 | 14634: contig of 832 bp in length |
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| * | 15572 | 15571: contig of 837 bp in length |
| * | 15672 | 15671: gap of 100 bp |
| * | 16505 | 16504: contig of 833 bp in length |
| * | 16605 | 16604: gap of 100 bp |
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| * | 18328 | 18327: contig of 834 bp in length |
| * | 18428 | 18427: gap of 100 bp |
| * | 19260 | 19259: contig of 832 bp in length |
| * | 19360 | 19359: gap of 100 bp |
| * | 20209 | 20208: contig of 849 bp in length |
| * | 20309 | 20308: gap of 100 bp |
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| * | 21242 | 20260: contig of 819 bp in length |

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| * | 22161 | contig of 100 bp |
| * | 22967 | gap of 100 bp |
| * | 23067 | contig of 803 bp in length |
| * | 23870 | gap of 100 bp |
| * | 23969 | gap of 100 bp |
| * | 24798 | contig of 829 bp in length |
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| * | 24899 | gap of 100 bp |
| * | 24899 | contig of 804 bp in length |
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| * | 25703 | gap of 100 bp |
| * | 25802 | gap of 100 bp |
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| * | 26568 | gap of 100 bp |

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 * 61630 62460: contig of 831 bp in length
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Query Match 55.9%; Score 306.2; DB 2; Length 70679;
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QY 252 TCAAAAGCAAAATGCCACCTTAGATCCCGGTCAATTTCTTCTCAGGAACCCCAATGAT 311
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QY 312 AAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGGTTAACTGAATACAGA 371
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QY 372 TTAGTCTCCATCAATAAAGCAGTCTCTTCAAAACCACTTCCTGCAATCATCTCAGAA 431
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Db 51773 GATGCTCCGGATATTGACAGCTCTGGGTGACACTTTGTCCCATCTGTGTACACC 51832

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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 24771)
 AUTHORS Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
 Yi,Q. and Nickerson,D.A.
 TITLE Direct Submission
 JOURNAL Submitted (15-JUN-2001) Molecular Biotechnology, University of
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA
 REFERENCE 2 (bases 1 to 24771)
 AUTHORS Rieder,M.J. and Nickerson,D.A.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2001) Molecular Biotechnology, University of
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA
 REMARK
 COMMENT On Jul 20, 2001 this sequence version replaced gi:14583134.
 To cite this work please use: SeattleSNPs. NHLBI Program for
 Genomic Applications, UW-FHRC, Seattle, WA (URL:

| FEATURES | source | http://pga.mbt.washington.edu/ |
|---------------------|---|--|
| Location/Qualifiers | 1. .24771 | |
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| variation | /frequency="0.07" /replace="C" | /frequency="0.22" /replace="C" |
| variation | 352 /frequency="0.42" /replace="A" | 2940 /gene="F2R" /frequency="0.01" /replace="G" |
| variation | 636 /frequency="0.01" /replace="A" | 2952 /gene="F2R" /frequency="0.01" /replace="T" |
| variation | 709 /frequency="0.02" /replace="T" | 3252 /gene="F2R" /frequency="0.01" /replace="C" |
| repeat_region | 811..1058 /rpt_family="AluJb" /rpt_type=dispersed | 3481 /gene="F2R" /frequency="0.39" /replace="C" |
| variation | 1184 /frequency="0.01" /replace="G" | 3525 /gene="F2R" /frequency="0.10" /replace="T" |
| variation | 1631..1643 /frequency="0.64" /replace="" | 3941..4047 /rpt_family="MIR" /rpt_type=dispersed |
| misc_feature | 1645..2063 /note="Region not scanned for variation" | 3948 /gene="F2R" /frequency="0.21" /replace="G" |
| gene | 1807..21315 /gene="F2R" | 4017 /gene="F2R" /frequency="0.24" /replace="C" |
| mRNA | Join(1807..2237,18156..21315) /gene="F2R" | 4038 /gene="F2R" /frequency="0.03" /replace="A" |
| variation | /product="coagulation factor II (thrombin) receptor" 2081 /gene="F2R" | 4087 /gene="F2R" /frequency="0.02" /replace="T" |
| CDS | /codon_start=1 /product="coagulation factor II (thrombin) receptor" /protein_id="AAK69768.1" /db_xref="GI:14583135" /translation="MGPRRLLLVAACFSLCGPLLSARTRARRPESKATNATLDRSFL LRNNDKYEPWDEEKNEGLTEVRLVSIKNSPLOKLPAPFISEDASGYLTSSWLT LFVPSVYGVFVSLPLNIMAIUVFILKMKYKPAVYMLHLATADLVFVSLVPFKIS YFSGSDWQFSGSELGRFVTAIFYCNMYASILLMTVISIDRFVAVVPMQSLSWRTLGR ASFTCLAIWALAIAGVPELLKEQTIQVPGNITTDHDLNETLLEGYIAYYFSAFSA VFVFPVLIISTVCVSIIRCLSSAVANRKSRAFLSAAVFCIFICFGPTNLLI AHYSLHTSTTEAAYFAYLLCVCVSSISCCIDPLIYYASSEQQRVYVYSLCKESS DPSSYSSGQLMASKMDTCSSNLNNSIYKLLT" | 4107 /gene="F2R" /frequency="0.03" /replace="T" |
| variation | /gene="F2R" /frequency="0.01" /replace="A" | 4336 /gene="F2R" /frequency="0.41" /replace="A" |
| variation | /gene="F2R" /frequency="0.05" /replace="A" | 4393 /gene="F2R" /frequency="0.03" /replace="A" |
| variation | 2372 /gene="F2R" /frequency="0.01" /replace="A" | 4617 /gene="F2R" /frequency="0.07" /replace="T" |
| variation | 2502 /gene="F2R" /frequency="0.01" /replace="A" | 4925 /gene="F2R" /frequency="0.01" /replace="G" |
| variation | 2762 /gene="F2R" /frequency="0.06" /replace="T" | 4971..5125 /rpt_family="MIR" /rpt_type=dispersed |
| variation | 2860 /gene="F2R" /frequency="0.40" /replace="A" | 5072 /gene="F2R" /frequency="0.01" /replace="C" |
| variation | 2930 /gene="F2R" | 5128 /gene="F2R" /frequency="0.22" /replace="G" |
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/replace="A"
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5515
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55.1%; Score 302; DB 9; Length 24771;
Best Local Similarity 100.0%; Pred. No. 7.6e-57;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 CAGAAATCAAAGCAAAATGCCACCTTAGATCCCGGTCAATTTCTTCTCAGGAACCCCA 306
Db |||||||
18153 CAGAAATCAAAGCAAAATGCCACCTTAGATCCCGGTCAATTTCTTCTCAGGAACCCCA 18212
QY |||||||
307 ATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAAATGAAAGTGGGTTAACTGAAT 366
Db |||||||
18213 ATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAAATGAAAGTGGGTTAACTGAAT 18272
QY |||||||
367 ACAGATTAGTCTCCATCAATAAAGCAGTCTCTTTCAAAAACAACTTCTCGCATTCATCT 426
Db |||||||
18273 ACAGATTAGTCTCCATCAATAAAGCAGTCTCTTTCAAAAACAACTTCTCGCATTCATCT 18332
QY |||||||
427 CAGAGATGCTCCGGATATTGACCAAGTCTCGGCTGACACTCTTTGTGCCATCTGTGT 486
Db |||||||
18333 CAGAGATGCTCCGGATATTGACCAAGTCTCGGCTGACACTCTTTGTGCCATCTGTGT 18392
QY |||||||
487 ACACCGGAGTGTGTGTAGTCAGCTCCCACTAAACATCATGGCCATCGTTGTGTTCAATCC 546
Db |||||||
18393 ACACCGGAGTGTGTGTAGTCAGCTCCCACTAAACATCATGGCCATCGTTGTGTTCAATCC 18452
QY ||
547 TG 548
Db ||
18453 TG 18454
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Search completed: December 20, 2003, 22:56:47
Job time : 2385 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2003, 21:53:50 ; Search time 1751 Seconds

(without alignments)
7606.427 Million cell updates/sec

Title: US-09-744-679-7

Perfect score: 548

Sequence: 1 cgcgcaggtcgcttgacc.....ccatcgtgtgttcacctg 548

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_esthum:*

3: em_estm:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 548 | 100.0 | 888 | 13 | B0440574 |
| 2 | 536 | 97.8 | 699 | 10 | B258615 |
| 3 | 505.2 | 92.2 | 739 | 10 | B473471 |
| 4 | 251.2 | 45.8 | 1072 | 13 | BUI73240 |

ALIGNMENTS

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RESULT 1
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LOCUS      AGENCOURT_7907353 NIH_MGC_67 Homo sapiens cdna clone IMAGE:6154861
DEFINITION AGENCOURT_7907353 NIH_MGC_67 Homo sapiens cdna clone IMAGE:6154861
5', mRNA Sequence.
ACCESSION  B0440574
VERSION    B0440574.1 GI:21179650
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 888)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L14M13496 row: j column: 14
            High quality sequence stop: 654.

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5 197 35.9 496 11 BC016059
6 184 33.6 457 14 CA892151
7 184 33.6 575 14 CA892359
8 184 33.6 997 13 B0839951
9 183 33.4 519 4 BX512139
10 183 33.4 621 10 BB662299
11 183 33.4 642 14 BY754069
12 183 33.4 658 14 BY753574
13 183 33.4 674 12 B1685426
14 183 33.4 676 14 BY754521
15 183 33.4 942 13 BQ96389
16 183 33.4 3338 11 AK085990
17 182.4 33.3 461 14 CA566568
18 182.4 33.3 492 14 CD554710
19 182.4 33.3 949 13 BQ923464
20 182 33.2 705 14 BY737790
21 181.4 33.1 513 14 CD554324
22 180.8 33.0 584 12 B1738768
23 175.8 32.1 688 9 AA882290
24 169.2 30.9 1031 13 BU516402
25 168.4 30.7 456 14 CA877850
26 166 30.3 445 14 CA880312
27 165.6 30.2 672 10 BE911999
28 164.2 30.0 709 13 BU611590
29 162.2 29.6 763 12 B1666195
30 159.2 29.1 467 10 BB862683
31 157.6 28.8 466 10 BB852109
32 152.2 27.8 410 13 BY228821
33 152 27.7 1429 13 BQ926183
34 145.8 26.6 405 10 BF116952
35 136.2 24.9 403 13 BY301816
36 135.8 24.8 374 14 CA876551
37 135.8 24.8 461 14 CA878584
38 135.2 24.7 411 13 BY109295
39 133.6 24.4 413 13 BY228431
40 133 24.3 557 10 BG067569
41 132.6 24.2 412 13 BY228469
42 132 24.1 554 14 C87335
43 132 24.1 588 14 C86764
44 130.8 23.9 399 13 BY228641
45 128 23.4 504 9 AA690768

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CA892359 B017SG06-
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BX512139 R2PD Mus
BB662299 BB662299
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BY753574 BY753574
B1685426 603308867
BY754521 BY754521
BQ96389 AGENCOURT
AK085990 Mus muscu
CA566568 K0402H07-
CD554710 B0381D04-
BQ923464 AGENCOURT
BY737790 BY737790
CD554324 B0374E01-
B1738768 603362614
AA882290 Vx43B01.r
BU516402 AGENCOURT
CA877850 K0960H08-
CA880312 K0981H11-
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BU611590 UI-M-F10-
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BF116952 UY92H02.Y
BY301816 BX301816
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CA878584 K0968B09-
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BY228469 BY228469
C87335 C87335 Mous
C86764 C86764 Mous
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/db_xref="taxon:9606"
/clone="IMAGE:6154861"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/notes="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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ORIGIN
Query Match 100.0%; Score 548; DB 13; Length 888;
Best Local Similarity 100.0%; Pred. No. 3.1e-131;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGAGGGTCGCTTGGACCTGATCTTACCGTGGGACCCCTCGCTTGCCTGCGCG 60
Db 25 CGCGAGGGTCGCTTGGACCTGATCTTACCGTGGGACCCCTCGCTTGCCTGCGCG 84
QY 61 AAGACCCGGCTCCCGACCCGAGAGGTGAGGAGAGAGGTGAGGAGAGAGCCCGAGGC 120
Db 85 AAGACCCGGCTCCCGACCCGAGAGGTGAGGAGAGAGGTGAGGAGAGAGCCCGAGGC 144
QY 121 GGGGAGCCTCCCGAGAGAGCCCGGAGAGCCCGGAGCAATGGGCGCGCGGCTGC 180
Db 145 GGGGAGCCTCCCGAGAGAGCCCGGAGAGCCCGGAGCAATGGGCGCGCGGCTGC 204
QY 181 TGCTGTGGCGGCTGCTTCAGTCTGTGGCGCGGCTGTGTCTGCGCGACCCGGGCC 240
Db 205 TGCTGTGGCGGCTGCTTCAGTCTGTGGCGCGGCTGTGTCTGCGCGACCCGGGCC 264
QY 241 GCAGGCGAGAAATCAAAAGCAACAAATGCCACTTACCTTACCTTCCCTCAGGA 300
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QY 301 ACCCCATGATTAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGTTAA 360
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QY 421 TCATCTCAGAGATGCTCCGGATATTGACCACTCTGCTGACACTCTTTGTCCCAT 480
Db 445 TCATCTCAGAGATGCTCCGGATATTGACCACTCTGCTGACACTCTTTGTCCCAT 504
QY 481 CTGTGTACCCGGAGTGTGTGTAGTACCTCCCACTAAACATCATGGCCATGTTGT 540
Db 505 CTGTGTACCCGGAGTGTGTGTAGTACCTCCCACTAAACATCATGGCCATGTTGT 564
QY 541 TCATCTCTG 548
Db 565 TCATCTCTG 572
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LOCUS
DEFINITION BE258615 699 bp mRNA linear EST 13-JUL-2000
601106874F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343051 5',
mRNA sequence.
ACCESSION BE258615
VERSION BE258615.1 GI:9129107
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QY 540 TTGATCTGT 548
Db 591 TTCATCTGT 599

RESULT 3
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LOCUS 602516274F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4647883 5',
DEFINITION mRNA sequence.
ACCESSION BG473471
VERSION BG473471.1 GI:13405746
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 739)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1425 row: C column: 20
High quality sequence stop: 718.
Location/Qualifiers
1. .739
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 16"
/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally-
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 162 a 207 c 200 g 170 t
ORIGIN
Query Match 92.2%; Score 505.2; DB 10; Length 739;
Best Local Similarity 99.1%; Pred. No. 3.7e-120;
Matches 529; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 16 GGACCTGATCTTACCGTGGGACACCTGGCTCTGCTCCGCGAGACCGGCTCCCG 75
Db 2 GGACCTGATCTTACCGTGGGACACCTGGCTCTGCTCCGCGAGACCGGCTCCCG 61

QY 76 ACCCGCAGAGTCAGGAGAGGGTGAAGCGGAGCAGCCGAGCGGGGCGAGCTCCCG 135
Db 62 ACCCGCAGAGTCAGGAGAGGGTGAAGCGGAGCAGCCGAGCGGGGCGAGCTCCCG 121

QY 136 AGCAGCGCGCGCAGAGCGCGGACAAATGGGCGCGCGCTGCTGCTGGTGGCGGCT 195
Db 122 AGCAGCGCGCGCAGAGCGCGGACAAATGGGCGCGCGCTGCTGCTGGTGGCGGCT 181

QY 196 GCTTCACTGTGTGCGCGCGCTGTTCTGTCCCGGACCCGCGGCGCGCAGGCGAATCAA 255
Db 182 GCTTCACTGTGTGCGCGCGCTGTTCTGTCCCGGACCCGCGGCGCGCAGGCGAATCAA 241

QY 256 AAGCAACAAATGCACCTTAGATCCCGGCTCATTTCTCTAGGAGACCCCAATGATAT 315
Db 256 AAGCAACAAATGCACCTTAGATCCCGGCTCATTTCTCTAGGAGACCCCAATGATAT 315

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Db 242 AAGCAACAAATGCACCTTAGATCCCGGCTCATTTCTCTAGGAGACCCCAATGATAAT 301
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Db 302 ATGAACCAATTTTGGAGGATGAGGAGAAAATGAAGTGGGTTAACTGAATACAGATTAG 361
QY 376 TCTCCATCAATAAAGCAGTCCTCTTCCAAAACAACATTCC-TGCATTTCATCTCAGAAGAT 434
Db 362 TCTCCATCAATAAAGCAGTCCTCTTCCAAAACAACATTCC-TGCATTTCATCTCAGAAGAT 421
QY 435 GCCTCCGATATTGACCACTCTGCTGCTGACACTCTTTGTCCCATCTGTGTACACCGGA 494
Db 422 GCCTCCGATATTGACCACTCTGCTGCTGACACTCTTTGTCCCATCTGTGTACACCGGA 481
QY 495 GTGTTGTAGTCAGCCTCCCACTAAACATCATGCGCATCGTTGTGTTTCATCTG 548
Db 482 GTG-TTGTAGTCAGCCTCCCACTAAACATCATGCGCATCGTTGTGTTTCATCTG 534

RESULT 4
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LOCUS BUI73240
DEFINITION BUI73240 1072 bp mRNA linear EST 04-SEP-2002
ACCESSION AGENCOURT_7939641 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6172703
VERSION BUI73240
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1072)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM13543 row: A column: 24
High quality sequence stop: 149.
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/clone_lib="NIH MGC 67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
BASE COUNT 247 a 320 c 289 g 211 t 5 others
ORIGIN
Query Match 45.8%; Score 251.2; DB 13; Length 1072;
Best Local Similarity 92.2%; Pred. No. 3e-54;
Matches 273; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 1 CGCCGAGGCTCGCTTGGACCTTATCCCGTGGGACACCTGCGCTCTGCTGCGCG 60
Db 24 CGCCGAGGCTCGCTTGGACCTTATCCCGTGGGACACCTGCGCTCTGCTGCGCG 83

QY 61 AAGACCGGCTCCCGACCGCGAGAGTCAAGGAGAGGAGGAGAGCGGAGAGCGCGAGGC 120
Db 84 AAGACCGGCTCCCGACCGCGAGAGTCAAGGAGAGGAGGAGAGCGGAGAGCGCGAGGC 143

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QY 121 GGGGAGCCTCCGGAGCAGCGCGCGAGAGCCCGGCAATGGGCGCGGGCTGC 180
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QY 181 TGCTGTGGCGCGCTCTTCAGTCTGTGCGCGCGCTGTGTCTGCGCGCA-CCCGGGCC 239
Db 204 TGCTGTGGCGCTCTTCAGTCTGTGCGCGCGCTGTGTCTGCGCGCA-CCCGGGCC 263
QY 240 CGCAGCGCAGAAATCAAAAGCAAAATGCCACTTAGATCCCGGTCAATTTCT 295
Db 264 GGCAGGCANAATCAAAAGCAAAATGCCACTTAATCCCGGGTCATTTTCT 319

RESULT 5
LOCUS BC016059
DEFINITION Homo sapiens, Similar to coagulation factor II (thrombin) receptor,
clone IMAGE:4849569, mRNA.
ACCESSION BC016059
VERSION BC016059.1 GI:16359189
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 496)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcapps-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Kzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcleavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 34 Row: a Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6031164
This clone has the following problem: retained intron.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B-R"
/notes="Vector: pOTB7"
BASE COUNT 130 a 144 c 146 g 76 t
ORIGIN

Query Match 35.9%; Score 197; DB 11; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.6e-40;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 113 CCCGAGCGGGGAGCGCTCCCGGAGCAGCGCCGCGAGAGCCCGGGAACAATGGGGCCGCG 172
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5', mRNA sequence.
ACCESSION CA892151
VERSION CA892151.1 GI:27343700
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 457)
AUTHORS Piao,Y., Dudekula,D.B., Qian,Y., Martin,P.R., Aiba,K., Vescovi,A.L.
and Ko,W.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
cDNA Library (Long)
JOURNAL Unpublished
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0170 row: E column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 457
POLYA-No.

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/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
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National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref: Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Dr. Angelo L. Vescovi (Institute for Stem
Cell Research, Italy). Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTTCTAGATCGCGCGCGCTTTT-3'] from
2.0 Microgram of total RNA, treated with 14 DNA polymerase
I, and purified by ethanol-precipitation. The cDNAs were
ligated to lone-linker L1-Sal4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by

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| QY | 545 | CCTG 548 |
|--|---------------------------|---|
| Db | 424 | CCTG 427 |
| <p>RESULT 9</p> <p>BX512139 standard; RNA; EST; 519 BP.</p> <p>BX512139; AC XX</p> <p>BX512139.1 SV XX</p> <p>27-MAY-2003 (Rel. 75, Created) XX</p> <p>27-MAY-2003 (Rel. 75, Last updated, Version 1) DT XX</p> <p>RZPD Mus musculus cDNA clone IMAGE:337258 5' EST. DE XX</p> <p>EST; expressed sequence tag. XX</p> <p>Mus musculus (house mouse) XX</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; XX</p> <p>Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. XX</p> <p>[1] XX</p> <p>1-519 RN</p> <p>Heil O., Ebert L., Neubert P., Peters M., Radelof U., Schneider D., XX</p> <p>Korn B.; RA</p> <p>Submitted (28-MAY-2003) to the EMBL/GenBank/DDAJ databases. RT</p> <p>RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer RL</p> <p>feld 580, D-69120 Heidelberg, Germany XX</p> <p>RZPD; IMAGE952C114. CC</p> <p>RZPDLIB; I.M.A.G.E. cDNA Clone Collection; CC</p> <p>Mouse UnigeneSet - RZPD2 (RZPDLIB No.981) CC</p> <p>http://www.rzpd.de/Clonecards/cgi-bin/showLib.pl.cgi/response?libNo=981 CC</p> <p>Contact: Ina Rofls CC</p> <p>RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH CC</p> <p>Heubnerweg 6, D-14059 Berlin, Germany CC</p> <p>Tel: +49 30 32639 101 CC</p> <p>Fax: +49 30 32639 111 CC</p> <p>www.rzpd.de CC</p> <p>This clone is available royalty-free from RZPD; CC</p> <p>contact RZPD (clone@rzpd.de) for further information. CC</p> <p>Seq primer: T7, Primer sequence: TAATACGACTCACTATAGG CC</p> | | |
| XX | Key | Location/Qualifiers |
| XX | source | 1..519 |
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| XX | | primer [5' |
| XX | | GTATTCACATCGAAGTGGAGCGCGCATGTTTTTTTTTTTTTTT 3'] |
| XX | | total mouse RNA [provided by Minoru Ko, Wayne State Univ.] |
| XX | | double-stranded cDNA was ligated to EcoRI adaptors |
| XX | | 5'-AATTCGGCAGCGAGG-3' and 5'-CCTCGTCCG-3' (Pharmacia), |
| XX | | digested with NotI and cloned into the NotI and EcoRI sites |
| XX | | of the p7T73D-Paci vector. Library went through one round |
| XX | | of normalization, and was constructed by Bento Soares and |
| XX | | M.Fatima Bonaldo." |
| XX | | /organism="Mus musculus" |
| XX | | /clone="IMAGE952C114" |
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| XX | Best Local Similarity | 65.3%; Pred. No. 1.1e-36; |
| XX | Matches 292; Conservative | 0; Mismatches 140; Indels 15; Gaps 1; |

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2003, 22:13:05 ; Search time 59 Seconds

(without alignments)
4099.626 Million cell updates/sec

Title: US-09-744-679-7

Perfect score: 548

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 548 | 100.0 | 3480 | 1 | US-07-657-769B-68 |
| 3 | 548 | 100.0 | 3480 | 1 | US-07-789-184-219 |
| 4 | 548 | 100.0 | 3480 | 1 | US-08-475-263-219 |
| 5 | 548 | 100.0 | 3480 | 1 | US-08-485-886-219 |
| 6 | 548 | 100.0 | 3480 | 2 | US-08-477-362-219 |
| 7 | 548 | 100.0 | 3480 | 2 | US-08-477-134-219 |
| 8 | 548 | 100.0 | 3480 | 3 | US-08-473-489A-219 |
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| | 43 | 37.2 | 6.8 | 1910 | 4 | US-09-149-476-297 | Sequence 297, App |
| | 44 | 37.2 | 6.8 | 1945 | 4 | US-09-149-476-164 | Sequence 164, App |
| | 45 | 37 | 6.8 | 2065 | 3 | US-08-335-865J-8 | Sequence 8, Appl |

ALIGNMENTS

RESULT 1
US-09-016-434-1328
; Sequence 1328, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION NUMBER: US/09/016,434
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1328:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G339676
US-09-016-434-1328

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Best Local Similarity 100.0%; Pred. No. 2.3e-134;

Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 68, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; STREET: 755 Page Mill Road

Query Match 100.0%; Score 548; DB 1; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGAGGGTGGACCCCTGATCTTACCGTGGGCAACCTTGGCTTGGCTGCGCGG 60
Db |||||
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Qy 61 AAGACCGGCTCCCGACCGCAGAGGTGAGGAGAGGTTGAAGCGGAGCGCCGAGGC 120
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Qy 124 AAGACCGGCTCCCGACCGCAGAGGTGAGGAGAGGTTGAAGCGGAGCGCCGAGGC 183
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; Patent No. 568768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road

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; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 219:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1499
; US-07-789-184-219

Query Match 100.0%; Score 548; DB 1; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 64 CGCCGAGGGTCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCGCTGCGCGG 123
QY 61 AAGACCGGGTCCCGACCCGAGAGGGGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAG 120
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Db 544 CTGTGTACACCGAGAGTGTGTAGTCAGAGCTCCCACTTAACATCATGGCATGTTGTGT 603
QY 541 TCATCCTG 548
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; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 219:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1499
; US-08-475-263-219

Query Match 100.0%; Score 548; DB 1; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGAGGGTCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCGCTGCGCGG 60
Db 64 CGCCGAGGGTCGCTTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCGCTGCGCGG 123
QY 61 AAGACCGGGTCCCGACCCGAGAGGGGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAG 120
Db 124 AAGACCGGGTCCCGACCCGAGAGGGGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAG 183
QY 121 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 184 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
QY 181 TGCTGTGGCGCGCTGCTTTCAGTCTGTGTGGCGCGCGCTGTGTGTGTGTGTGTGTGT 240
Db 244 TGCTGTGGCGCGCTGCTTTCAGTCTGTGTGGCGCGCGCTGTGTGTGTGTGTGTGTGT 303
QY 241 GCAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 304 GCAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
QY 301 ACCCAATGATTAATGATGACCAATTTGGGAGAGATGAGGAGAGAGAGAGAGAGAG 360
Db 364 ACCCAATGATTAATGATGACCAATTTGGGAGAGATGAGGAGAGAGAGAGAGAGAG 423
QY 361 CTGAATACAGATAGTCTCCATCAATAAAGAGAGTCTCTTCAAAAACAACTTCTTGCAT 420
Db 424 CTGAATACAGATAGTCTCCATCAATAAAGAGAGTCTCTTCAAAAACAACTTCTTGCAT 483
QY 421 TCATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 484 TCATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
QY 481 CTGTGTACACCGAGAGTGTGTAGTCAGAGCTCCCACTTAACATCATGGCATGTTGTGT 540
Db 544 CTGTGTACACCGAGAGTGTGTAGTCAGAGCTCCCACTTAACATCATGGCATGTTGTGT 603
QY 541 TCATCCTG 548
```

QY 301 ACCCAATGATAAATATGAACCAATTTTGGAGGATGAGGAGAAAATGAAAGTGGTTAA 360
Db 364 ACCCAATGATAAATATGAACCAATTTTGGAGGATGAGGAGAAAATGAAAGTGGTTAA 423
QY 361 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACTTCTGCAAT 420
Db 424 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACTTCTGCAAT 483
QY 421 TCATCTCAGAAGATCCCTCCGGATATTTGACAGCTCCTGGTGACACTCTTTTGTCCCAT 480
Db 484 TCATCTCAGAAGATCCCTCCGGATATTTGACAGCTCCTGGTGACACTCTTTTGTCCCAT 543
QY 481 CTGTGTACACCGAGTGTGTGTGAGTCAAGTCCCTCCCAATAACATCATGCGCATGTTGTGT 540
Db 544 CTGTGTACACCGAGTGTGTGTGAGTCAAGTCCCTCCCAATAACATCATGCGCATGTTGTGT 603
QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 5

US-08-485-886-219 Application US/08485886
; Sequence 219, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1499
; US-08-485-886-219

Query Match 100.0%; Score 548; DB 1; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGAGGAGTGGTGGACCTGATCTTTACCGTGGGACACCTCGCTGCTGCTGCTGCGCG 60
Db 64 CGCGAGGAGTGGTGGACCTGATCTTTACCGTGGGACACCTCGCTGCTGCTGCTGCGCG 123
QY 61 AAGACCGGCTCCCGACCCCGAGAGTCAAGGAGAGGAGTGAAGCGAGAGAGAGAGAGG 120
Db 124 AAGACCGGCTCCCGACCCCGAGAGTCAAGGAGAGGAGTGAAGCGAGAGAGAGAGAGG 183
QY 121 GGGGAGGAGTCCCGAG 180
Db 184 GGGGAGGAGTCCCGAG 243
QY 181 TGCTGTGGCGGCTGCTTCAAGTCTGTGCGGCGCGCTGTGCTGCGCGAGAGAGAGAGAG 240
Db 244 TGCTGTGGCGGCTGCTTCAAGTCTGTGCGGCGCGCTGTGCTGCGCGAGAGAGAGAG 303
QY 241 GCAGGCCAGAATCAAAAGCAAAATGACCACTTTAGATCCCGGTCATTTCTTCTCAGGA 300
Db 304 GCAGGCCAGAATCAAAAGCAAAATGACCACTTTAGATCCCGGTCATTTCTTCTCAGGA 363
QY 301 ACCCAATGATAAATATGAACCAATTTTGGAGGATGAGGAGAAAATGAAAGTGGTTAA 360
Db 364 ACCCAATGATAAATATGAACCAATTTTGGAGGATGAGGAGAAAATGAAAGTGGTTAA 423
QY 361 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACTTCTGCAAT 420
Db 424 CTGAATACAGATTAGTCTCCATCAATAAAGCAGTCTCTTCAAAAACAACTTCTGCAAT 483
QY 421 TCATCTCAGAAGATCCCTCCGGATATTTGACAGCTCCTGGTGACACTCTTTTGTCCCAT 480
Db 484 TCATCTCAGAAGATCCCTCCGGATATTTGACAGCTCCTGGTGACACTCTTTTGTCCCAT 543
QY 481 CTGTGTACACCGAGTGTGTGTGAGTCAAGTCCCTCCCAATAACATCATGCGCATGTTGTGT 540
Db 544 CTGTGTACACCGAGTGTGTGTGAGTCAAGTCCCTCCCAATAACATCATGCGCATGTTGTGT 603
QY 541 TCATCCTG 548
Db 604 TCATCCTG 611

RESULT 6

US-08-477-362-219
; Sequence 219, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

Db 544 CTGTGTACCGAGTGTGTAGTCAGCTCCCACTAAACATCATGSCCATCGTTGTGT 603
Qy 541 TCATCTGT 548
Db 604 TCATCTGT 611

RESULT 8
US-08-473-489A-219
; Sequence 219, Application US/08473489A
; Patent No. 6024936
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,489A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 1991-11-07
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1499
; US-08-473-489A-219

Query Match 100.0%; Score 548; DB 3; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGAGGGTGGTGGACCTGATCTTACCGTGGGCGACCTCGCTCGCTCGCGCG 60
Db 64 CGCGAGGGTGGTGGACCTGATCTTACCGTGGGCGACCTCGCTCGCTCGCGCG 123
Qy 61 AAGACCGGCTCCCGACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 124 AAGACCGGCTCCCGACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
Qy 121 GGGGAGCGCTCCCGAG 180
Db 184 GGGGAGCGCTCCCGAG 243
Qy 181 TGCTGGTGGCGCGCTGCTTTCAGTGTGTGTGGCGCGCGCTGTTGTCTGCCCGCACCGCGGCC 240

Db 244 TGCTGGTGGCGCGCTGCTTTCAGTGTGTGTGGCGCGCGCTGTTGTCTGCCCGCACCGCGGCC 303
Qy 241 GCAGGCGAGAGTCAAAAGAGCAAAATGCCACCTTAGATCCCGGTCAATTTCTTCTCAGGA 300
Db 304 GCAGGCGAGAGTCAAAAGAGCAAAATGCCACCTTAGATCCCGGTCAATTTCTTCTCAGGA 363
Qy 301 ACCCAATGATAAATATGAAACCAATTTTGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 364 ACCCAATGATAAATATGAAACCAATTTTGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 423
Qy 361 CTGAATACAGATTAGTCTCCATCAATAAAGAGAGTCTCTTCAAAAAACAATTCCTGCAT 420
Db 424 CTGAATACAGATTAGTCTCCATCAATAAAGAGAGTCTCTTCAAAAAACAATTCCTGCAT 483
Qy 421 TCATCTCAGAAGATGCTCCGATATTTGACAGCTCTCGGTGACACTCTTTGTGCCAT 480
Db 484 TCATCTCAGAAGATGCTCCGATATTTGACAGCTCTCGGTGACACTCTTTGTGCCAT 543
Qy 481 CTGTGTACACGGAGTGTGTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 540
Db 544 CTGTGTACACGGAGTGTGTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 603
Qy 541 TCATCTGT 548
Db 604 TCATCTGT 611

RESULT 9
US-08-485-695-219
; Sequence 219, Application US/08485695
; Patent No. 6124101
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,695
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

LOCATION: 225..1499
US-08-485-695-219

Query Match 100.0%; Score 548; DB 3; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGAGGGTGGTGGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG 60
DB 64 CGCGAGGGTGGTGGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG 123

QY 61 AAGACCGGCTCCCGACCGGACAGTTCAGAGAGGGTGAAGGGAGAGCCCGAGGC 120
DB 124 AAGACCGGCTCCCGACCGGACAGTTCAGAGAGGGTGAAGGGAGAGCCCGAGGC 183

QY 121 GGGGAGCGCTCCCGAGGAGCGCGGACAGCCCGGACAAATGGGGCGCGGGCTGC 180
DB 184 GGGGAGCGCTCCCGAGGAGCGCGGACAGCCCGGACAAATGGGGCGCGGGCTGC 243

QY 181 TGCTGGTGGCGCTGCTTCAATGATCTGTGCGCGCGCTGTGCTGCGCGCGCGGCC 240
DB 244 TGCTGGTGGCGCTGCTTCAATGATCTGTGCGCGCGCTGTGCTGCGCGCGGCC 303

QY 241 GCAGCCAGAAATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 300
DB 304 GCAGCCAGAAATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 363

QY 301 ACCCAATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGTTAA 360
DB 364 ACCCAATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGTTAA 423

QY 361 CTGAATACAGATTAGTCTCCATCAATCAAAAGCAGTCTCTTCAAAACAACTTCTGCAT 420
DB 424 CTGAATACAGATTAGTCTCCATCAATCAAAAGCAGTCTCTTCAAAACAACTTCTGCAT 483

QY 421 TCATCTCAGAGATGCGCTCCGATATTTGACAGCTCTGCTGACACTCTTTGTCCTCAT 480
DB 484 TCATCTCAGAGATGCGCTCCGATATTTGACAGCTCTGCTGACACTCTTTGTCCTCAT 543

QY 481 CTGTGTACCCGAGATGTTTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 540
DB 544 CTGTGTACCCGAGATGTTTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 603

RESULT 10
US-08-018-760-219
Sequence 219, Application US/08018760
Patent No. 6197541
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,760
FILING DATE: 17-FEB-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 3480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1499
US-08-018-760-219

Query Match 100.0%; Score 548; DB 3; Length 3480;
Best Local Similarity 100.0%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGAGGGTGGTGGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG 60
DB 64 CGCGAGGGTGGTGGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG 123

QY 61 AAGACCGGCTCCCGACCGGACAGTTCAGAGAGGGTGAAGGGAGAGCCCGAGGC 120
DB 124 AAGACCGGCTCCCGACCGGACAGTTCAGAGAGGGTGAAGGGAGAGCCCGAGGC 183

QY 121 GGGGAGCGCTCCCGAGGAGCGCGGACAGCCCGGACAAATGGGGCGCGGGCTGC 180
DB 184 GGGGAGCGCTCCCGAGGAGCGCGGACAGCCCGGACAAATGGGGCGCGGGCTGC 243

QY 181 TGCTGGTGGCGCTGCTTCAATGATCTGTGCGCGCGCTGTGCTGCGCGCGCGGCC 240
DB 244 TGCTGGTGGCGCTGCTTCAATGATCTGTGCGCGCGCTGTGCTGCGCGCGGCC 303

QY 241 GCAGCCAGAAATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 300
DB 304 GCAGCCAGAAATCAAAAGCAAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 363

QY 301 ACCCAATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGTTAA 360
DB 364 ACCCAATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAATGAAAGTGGTTAA 423

QY 361 CTGAATACAGATTAGTCTCCATCAATCAAAAGCAGTCTCTTCAAAACAACTTCTGCAT 420
DB 424 CTGAATACAGATTAGTCTCCATCAATCAAAAGCAGTCTCTTCAAAACAACTTCTGCAT 483

QY 421 TCATCTCAGAGATGCGCTCCGATATTTGACAGCTCTGCTGACACTCTTTGTCCTCAT 480
DB 484 TCATCTCAGAGATGCGCTCCGATATTTGACAGCTCTGCTGACACTCTTTGTCCTCAT 543

QY 481 CTGTGTACCCGAGATGTTTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 540
DB 544 CTGTGTACCCGAGATGTTTGTAGTACGCTCCCACTAAACATCATGSCCATCGTTGTGT 603

QY 541 TCATCCTG 548
DB 604 TCATCCTG 611

RESULT 11
US-08-313-553-12
Sequence 12, Application US/08313553
Patent No. 5641650
GENERAL INFORMATION:

APPLICANT: TURNER, George J.
APPLICANT: BETLACH, Mary C.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
TITLE OF INVENTION: IN HALOBACTERIA
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,662
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57669/WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: repeat region
LOCATION: 435..462
OTHER INFORMATION: /note= "Sequence encoding
Patent No. 5641650
OTHER INFORMATION: polypartite acid."
FEATURE:
NAME/KEY: misc feature
LOCATION: 463..465
OTHER INFORMATION: /note= "Codon encoding the
OTHER INFORMATION: N-terminal amino acid of the human thrombin
OTHER INFORMATION: receptor protein."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1630..1632
OTHER INFORMATION: /note= "Codon encoding the
OTHER INFORMATION: C-terminal amino acid of the human thrombin
OTHER INFORMATION: receptor protein."
FEATURE:
NAME/KEY: repeat region
LOCATION: 1633..1650
OTHER INFORMATION: /note= "Sequence encoding
Patent No. 5641650
OTHER INFORMATION: polyhistidine."
FEATURE:
NAME/KEY: misc feature
LOCATION: 648..656
OTHER INFORMATION: /note= "Deleted AlwNI restriction
OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc feature
LOCATION: 893..898
OTHER INFORMATION: /note= "Deleted PstI restriction
OTHER INFORMATION: site."
FEATURE:

NAME/KEY: misc feature
LOCATION: 1301..1309
OTHER INFORMATION: /note= "Deleted AlwNI restriction
OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1394..1402
OTHER INFORMATION: /note= "Deleted AlwNI restriction
OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc_signal
LOCATION: 374
OTHER INFORMATION: /note= "RNA start site."
FEATURE:
NAME/KEY: mutation
LOCATION: replace(1671, "")
OTHER INFORMATION: /note= "C to T mutation removes
OTHER INFORMATION: AlwNI site."
FEATURE:
NAME/KEY: CDS
LOCATION: 376..1650
FEATURE:
NAME/KEY: misc feature
LOCATION: 376..414
OTHER INFORMATION: /note= "Bacteriorhodopsin
OTHER INFORMATION: pre-sequence."
FEATURE:
NAME/KEY: terminator
LOCATION: 1672..1674
OTHER INFORMATION: /note= "Bacteriorhodopsin stop
OTHER INFORMATION: codon."
FEATURE:
NAME/KEY: terminator
LOCATION: 1651..1653
OTHER INFORMATION: /note= "Thrombin stop codon."
US-08-313-553-12
Query Match 51.5%; Score 282.4; DB 1; Length 1764;
Best Local Similarity 99.6%; Pred. No. 8.1e-65;
Matches 283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 265 ATGCCACCTTAGATCCCGGTTCATTTCTTCTCAGAAACCCCAATGATAAATATGAACCAT 324
Db 461 ACGCCACCTTAGATCCCGGTTCATTTCTTCTCAGAAACCCCAATGATAAATATGAACCAT 520
Qy 325 TTTCGGAGGATGAGGAGAGAAAAATGAAAGTGGTTAACTGAATACAGATTAGTCTCCATCA 384
Db 521 TTTCGGAGGATGAGGAGAGAAAAATGAAAGTGGTTAACTGAATACAGATTAGTCTCCATCA 580
Qy 385 ATAAAGCAGTCTCTTCAAAAACAACCTTCTGCATTCTCAGAAAGATGCCCTCCCGAT 444
Db 581 ATAAAGCAGTCTCTTCAAAAACAACCTTCTGCATTCTCAGAAAGATGCCCTCCCGAT 640
Qy 445 ATTGACCACTCTCTGGCTGACACTCTTTGTCCCATCTGTGTACACCGGAGTGTGTAG 504
Db 641 ATTGACCACTCTCTGGCTGACACTCTTTGTCCCATCTGTGTACACCGGAGTGTGTAG 700
Qy 505 TCAGCTCCCACTAAACATCATGCCCATCTTGTGTTCATCTG 548
Db 701 TCAGCTCCCACTAAACATCATGCCCATCTTGTGTTCATCTG 744
RESULT 12
US-08-767-993-12
Sequence 12, Application US/08767993
Patent No. 6010885
GENERAL INFORMATION:
APPLICANT: TURNER, George J.
APPLICANT: BETLACH, Mary C.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
TITLE OF INVENTION: IN HALOBACTERIA
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,993
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57669/WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: repeat region
LOCATION: 436..462
OTHER INFORMATION: /note= "Sequence encoding
Patent No. 6010885
OTHER INFORMATION: polypeptidic acid."
FEATURE:
NAME/KEY: misc feature
LOCATION: 463..465
OTHER INFORMATION: /note= "Codon encoding the
OTHER INFORMATION: N-terminal amino acid of the human thrombin
OTHER INFORMATION: receptor protein."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1630..1632
OTHER INFORMATION: /note= "Codon encoding the
OTHER INFORMATION: C-terminal amino acid of the human thrombin
OTHER INFORMATION: receptor protein."
FEATURE:
NAME/KEY: repeat region
LOCATION: 1633..1650
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OTHER INFORMATION: polyhistidine."
FEATURE:
NAME/KEY: misc feature
LOCATION: 648..656
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OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc feature
LOCATION: 893..898
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OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1301..1309
OTHER INFORMATION: /note= "Deleted AlwNI restriction
OTHER INFORMATION: site."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1394..1402
OTHER INFORMATION: /note= "Deleted AlwNI restriction
OTHER INFORMATION: site."

FEATURE:
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LOCATION: 374
OTHER INFORMATION: /note= "RNA start site."
FEATURE:
NAME/KEY: mutation
LOCATION: replace(1671, "")
OTHER INFORMATION: /note= "C to T mutation removes
OTHER INFORMATION: AlwNI site."
FEATURE:
NAME/KEY: CDS
LOCATION: 376..1650
FEATURE:
NAME/KEY: misc feature
LOCATION: 376..414
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FEATURE:
NAME/KEY: terminator
LOCATION: 1672..1674
OTHER INFORMATION: /note= "Bacteriorhodopsin stop
OTHER INFORMATION: codon."
FEATURE:
NAME/KEY: terminator
LOCATION: 1651..1653
OTHER INFORMATION: /note= "Thrombin stop codon."
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Best Local Similarity 99.6%; Pred. No. 8.1e-65;
Matches 283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db |||||
Db 521 TTGGGAGATGAGGAGAAAATGAAGTGGTTAACTGAATACAGATTAGTCTCCATCA 580
QY 385 ATAAAGCAGTCCCTTTCAAAACCACTTCTGCAATTCATCTCAGAAGTGGCTCCGGAT 444
Db |||||
Db 581 ATAAAGCAGTCCCTTTCAAAACCACTTCTGCAATTCATCTCAGAAGTGGCTCCGGAT 640
QY 445 ATTGACCAAGTCCCTGGCTGACACTCTTTGTGCCATCTGTGTACACCGAGTGTGTAG 504
Db |||||
Db 641 ATTGACCAAGTCCCTGGCTGACACTCTTTGTGCCATCTGTGTACACCGAGTGTGTAG 700
QY 505 TCAGCTCCCACTAAACATCATGCGCATCGTGTGTTCATCTG 548
Db |||||
Db 701 TCAGCTCCCACTAAACATCATGCGCATCGTGTGTTCATCTG 744
RESULT 13
US-08-795-876-31
; Sequence 31, Application US/08795876
; Patent No. 6403305
; GENERAL INFORMATION:
; APPLICANT: Gershengorn, Marvin C.
; APPLICANT: Geras-Raaka, Elizabeth
; APPLICANT: Nussenzweig, Daniel R.
; TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
; TITLE OF INVENTION: COUPLED RECEPTORS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/795,876
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BRAMAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/1280
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1300 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-795-876-31

Query Match      22.9%; Score 125.4; DB 4; Length 1300;
Best Local Similarity 86.8%; Pred. No. 1.1e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 314 ATATGAACCATTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 373
Db 155 ATATGCCACCTTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 214
QY 374 AGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCAATTCATCTCAGAAGA 433
Db 215 AGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCAATTCATCTCAGAAGA 274
QY 434 TGCCTCCGATATTTCAGCAGTCCTCTGCTGCTGACATCTT 472
Db 275 TGCCTCCGTTACCTGGGTACAAATCCTCAGAGTCCT 313

RESULT 14
US-08-795-876-36
/ Sequence 36, Application US/08795876
/ Patent No. 6403305
/ GENERAL INFORMATION:
/ APPLICANT: Gershengorn, Marvin C.
/ APPLICANT: Geras-Raaka, Elizabeth
/ APPLICANT: Nussenzweig, Daniel R.
/ TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
/ TITLE OF INVENTION: COUPLED RECEPTORS
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
/ STREET: Clinton Square, P.O. Box 1051
/ CITY: Rochester
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BRAMAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/1280
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1300 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-795-876-31

Query Match      22.9%; Score 125.4; DB 4; Length 1300;
Best Local Similarity 86.8%; Pred. No. 1.1e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 314 ATATGAACCATTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 373
Db 155 ATATGCCACCTTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 214
QY 374 AGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCAATTCATCTCAGAAGA 433
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QY 434 TGCCTCCGATATTTCAGCAGTCCTCTGCTGCTGACATCTT 472
Db 275 TGCCTCCGTTACCTGGGTACAAATCCTCAGAGTCCT 313

RESULT 15
US-08-795-876-37/c
/ Sequence 37, Application US/08795876
/ Patent No. 6403305
/ GENERAL INFORMATION:
/ APPLICANT: Gershengorn, Marvin C.
/ APPLICANT: Geras-Raaka, Elizabeth
/ APPLICANT: Nussenzweig, Daniel R.
/ TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
/ TITLE OF INVENTION: COUPLED RECEPTORS
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
/ STREET: Clinton Square, P.O. Box 1051
/ CITY: Rochester
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BRAMAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/1280
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1300 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-795-876-37

Query Match      22.6%; Score 123.8; DB 4; Length 1300;
Best Local Similarity 86.2%; Pred. No. 2.9e-23;
Matches 137; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1300 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-795-876-36

Query Match      22.9%; Score 125.4; DB 4; Length 1300;
Best Local Similarity 86.8%; Pred. No. 1.1e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 314 ATATGAACCATTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 373
Db 155 ATATGCCACCTTTTGGGAGGATGAGGAGAAATGAAGTGGTTAACTGAATACAGATT 214
QY 374 AGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCAATTCATCTCAGAAGA 433
Db 215 AGTCTCCATCAATAAAAGCAGTCCTCTTCAAAAACAACCTTCTGCAATTCATCTCAGAAGA 274
QY 434 TGCCTCCGATATTTCAGCAGTCCTCTGCTGCTGACATCTT 472
Db 275 TGCCTCCGTTACCTGGGTACAAATCCTCAGAGTCCT 313

RESULT 15
US-08-795-876-37/c
/ Sequence 37, Application US/08795876
/ Patent No. 6403305
/ GENERAL INFORMATION:
/ APPLICANT: Gershengorn, Marvin C.
/ APPLICANT: Geras-Raaka, Elizabeth
/ APPLICANT: Nussenzweig, Daniel R.
/ TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
/ TITLE OF INVENTION: COUPLED RECEPTORS
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
/ STREET: Clinton Square, P.O. Box 1051
/ CITY: Rochester
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BRAMAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/1280
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1300 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-795-876-37

Query Match      22.6%; Score 123.8; DB 4; Length 1300;
Best Local Similarity 86.2%; Pred. No. 2.9e-23;
Matches 137; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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Search completed: December 20, 2003, 23:32:58
Job time : 61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2003, 21:56:50 ; Search time 258 Seconds
(without alignments)
7077.703 Million cell updates/sec

Title: US-09-744-679-7

Perfect score: 548
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Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 548 | 100.0 | 3592 | 15 | US-10-225-567A-323 |
| 2 | 548 | 100.0 | 3592 | 15 | US-10-177-293-129 |
| 3 | 445 | 81.2 | 3299 | 15 | US-10-208-408-24 |
| 4 | 387 | 70.6 | 1278 | 13 | US-10-176-464A-2 |
| 5 | 301.6 | 55.0 | 6203 | 13 | US-10-176-464A-1 |
| 6 | 236.2 | 43.1 | 405 | 11 | US-09-948-995-16689 |
| 7 | 148.2 | 27.0 | 6436 | 13 | US-10-311-455-654 |
| 8 | 146.6 | 26.8 | 6436 | 13 | US-10-311-455-653 |
| 9 | 102.4 | 18.7 | 1440 | 13 | US-10-176-464A-66 |
| 10 | 44.6 | 8.1 | 192 | 10 | US-09-925-664-33 |
| 11 | 44.4 | 8.1 | 897 | 13 | US-10-029-386-24941 |
| 12 | 43.2 | 7.9 | 309 | 15 | US-10-156-761-610 |
| 13 | 43.2 | 7.9 | 9025608 | 15 | US-10-156-761-1 |
| 14 | 42.4 | 7.7 | 846 | 15 | US-10-156-761-7276 |
| 15 | 42.4 | 7.7 | 9025608 | 15 | US-10-156-761-1 |

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| 16 | 42 | 7.7 | 1737 | 13 | US-10-029-386-25063 | Sequence 25063, A |
| 17 | 40.8 | 7.4 | 729 | 13 | US-10-027-632-126950 | Sequence 126950, |
| 18 | 40.8 | 7.4 | 729 | 14 | US-10-027-632-126950 | Sequence 126950, |
| 19 | 40.8 | 7.4 | 737 | 13 | US-10-027-632-16043 | Sequence 16043, A |
| 20 | 40.8 | 7.4 | 737 | 14 | US-10-027-632-16043 | Sequence 16043, A |
| 21 | 40.8 | 7.4 | 1323 | 15 | US-10-156-761-5360 | Sequence 5360, Ap |
| 22 | 40.6 | 7.4 | 189 | 10 | US-09-925-664-31 | Sequence 31, Appl |
| 23 | 40.6 | 7.4 | 9369 | 13 | US-10-200-582-190 | Sequence 190, App |
| 24 | 40.6 | 7.4 | 9369 | 13 | US-10-237-551-190 | Sequence 190, App |
| 25 | 40.6 | 7.4 | 9369 | 13 | US-10-237-551-247 | Sequence 247, App |
| 26 | 40.6 | 7.4 | 154746 | 13 | US-09-827-688-8 | Sequence 8, Appli |
| 27 | 40.4 | 7.4 | 1738 | 13 | US-10-029-386-25470 | Sequence 25470, A |
| 28 | 40.2 | 7.3 | 592 | 13 | US-10-027-632-126949 | Sequence 126949, |
| 29 | 40.2 | 7.3 | 592 | 14 | US-10-027-632-126949 | Sequence 126949, |
| 30 | 40.2 | 7.3 | 556 | 13 | US-10-027-632-105398 | Sequence 105398, |
| 31 | 40.2 | 7.3 | 556 | 14 | US-10-027-632-105398 | Sequence 105398, |
| 32 | 40.2 | 7.3 | 32195 | 9 | US-09-764-870-611 | Sequence 611, App |
| 33 | 40.2 | 7.3 | 32195 | 9 | US-09-764-870-617 | Sequence 617, App |
| 34 | 40.2 | 7.3 | 32195 | 9 | US-09-764-869-1605 | Sequence 1605, Ap |
| 35 | 40.2 | 7.3 | 32195 | 15 | US-10-125-540-611 | Sequence 611, App |
| 36 | 40.2 | 7.3 | 32195 | 15 | US-10-125-540-617 | Sequence 617, App |
| 37 | 40.2 | 7.3 | 32195 | 15 | US-10-091-584-1605 | Sequence 1605, Ap |
| 38 | 39.8 | 7.3 | 2793 | 13 | US-10-156-761-2889 | Sequence 2889, Ap |
| 39 | 39.8 | 7.3 | 125746 | 15 | US-10-156-761-15102 | Sequence 15102, A |
| 40 | 39.6 | 7.2 | 409 | 10 | US-09-960-352-13321 | Sequence 13321, A |
| 41 | 39.6 | 7.2 | 594 | 13 | US-10-140-472-10 | Sequence 10, Appl |
| 42 | 39.6 | 7.2 | 594 | 13 | US-10-141-761-10 | Sequence 10, Appl |
| 43 | 39.6 | 7.2 | 594 | 13 | US-10-142-885-10 | Sequence 10, Appl |
| 44 | 39.6 | 7.2 | 594 | 13 | US-10-158-790-10 | Sequence 10, Appl |
| 45 | 39.6 | 7.2 | 594 | 13 | US-10-137-871-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1

US-10-225-567A-323
; Sequence 323, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 323
; LENGTH: 3592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-323

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| Query Match | 100.0% | Score 548; | DB 15; | Length 3592; |
| Best Local Similarity | 100.0% | Pred. No. 7.7e-158; | | |
| Matches 548; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | CGCGAGGCTGCTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG | 60 | |
| Db | 184 | CGCGAGGCTGCTGACCCCTGATCTTACCGTGGGACCCCTGCGCTCTGCTGCGCGG | 243 | |
| Qy | 61 | AAGACCGCTCCCGACCCGACAGTTCAGAGAGAGGGTGAAGCGAGCGAGCCGAGCCGAGGC | 120 | |
| Db | 244 | AAGACCGCTCCCGACCCGACAGTTCAGAGAGAGGGTGAAGCGAGCGAGCCGAGGC | 303 | |
| Qy | 121 | GGGCGAGCTTCCCGAGAGAGCCGCGGAGAGCCCGGAGCAATGGGGCGCGCGGCTGC | 180 | |
| Db | 304 | GGGCGAGCTTCCCGAGAGAGCCGCGGAGAGCCCGGAGCAATGGGGCGCGCGGCTGC | 363 | |

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QY 181 TGCTGGTGGCGCGCTGCTTCACTGCTGCGCGCGCTGTTGTCTGCGCGCACCGCGGCC 240
Db |||
QY 364 TGCTGGTGGCGCGCTGCTTCACTGCTGCGCGCGCTGTTGTCTGCGCGCACCGCGGCC 423
Db |||
QY 241 GCAGCGCAGAAATCAAAAGCAACAAATGCGCAGCTTAGATGCGCGGTCAATTTCTTCAGGA 300
Db |||
QY 424 GCAGCGCAGAAATCAAAAGCAACAAATGCGCAGCTTAGATGCGCGGTCAATTTCTTCAGGA 483
Db |||
QY 301 ACCCAATGATAATATATCAACCATTTTGGGAGGATGAGGAGAAAAATGAAAGTGGGTAA 360
Db |||
QY 484 ACCCAATGATAATATATCAACCATTTTGGGAGGATGAGGAGAAAAATGAAAGTGGGTAA 543
Db |||
QY 361 CTGAATCAGATTTAGTCTCCATCAATAAAGAGCTCTTTCATAAAACAACTTCTTCAT 420
Db |||
QY 544 CTGAATCAGATTTAGTCTCCATCAATAAAGAGCTCTTTCATAAAACAACTTCTTCAT 603
Db |||
QY 421 TCATCTCAGAGATGCTCCGAGATTTTGACAGCTCTCTGCTGACACTCTTTTGTCCCAT 480
Db |||
QY 604 TCATCTCAGAGATGCTCCGAGATTTTGACAGCTCTCTGCTGACACTCTTTTGTCCCAT 663
Db |||
QY 481 CTGTGTACACCGGAGTGTGTTAGTCAAGCTCCCACTAAACATCATGSCCATCGTTGTGT 540
Db |||
QY 664 CTGTGTACACCGGAGTGTGTTAGTCAAGCTCCCACTAAACATCATGSCCATCGTTGTGT 723
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QY 541 TCATCCTG 548
Db |||
QY 724 TCATCCTG 731

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RESULT 2

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US-10-177-293-129
; Sequence 129, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: East Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129

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; LENGTH: 3592
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-177-293-129

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Query Match 100.0%; Score 548; DB 15; Length 3592;
Best Local Similarity 100.0%; Pred. No. 7.7e-158;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AGACCGGCTCCCGACCCGCGAGAGTCAAGAGAGAGGGTGAAGCGGAGAGAGCGGAGCGCGAGCG 120
Db |||
QY 244 AGACCGGCTCCCGACCCGCGAGAGTCAAGAGAGAGGGTGAAGCGGAGAGAGCGGAGCGCGAGCG 303
Db |||
QY 121 GGGGAGGCTCCCGAGGAGCGCGCGAGAGCCCGGAGCAATGGGGCGCGCGGCGCTGC 180
Db |||
QY 304 GGGGAGGCTCCCGAGGAGCGCGCGCGAGAGCCCGGAGCAATGGGGCGCGCGGCGCTGC 363
Db |||
QY 181 TGCTGTGCGCGCTCTTCACTGCTGTGCGCGCGCTGTTGTCTGCGCGCACCGCGGCGCC 240
Db |||
QY 364 TGCTGTGCGCGCTCTTCACTGCTGTGCGCGCGCTGTTGTCTGCGCGCACCGCGGCGCC 423
Db |||
QY 241 GCAGGCGAGAAATCAAAAGCAACAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 300
Db |||
QY 424 GCAGGCGAGAAATCAAAAGCAACAAATGCCACCTTAGATCCCGGCTCATTTCTTCAGGA 483
Db |||
QY 301 ACCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAATGAAAGTGGGTAA 360
Db |||
QY 484 ACCCAATGATAATATGAACCAATTTTGGGAGGATGAGGAGAAAAATGAAAGTGGGTAA 543
Db |||
QY 361 CTGAATCAGATTTAGTCTCCATCAATAAAGAGAGTCTCTTCAAAACAACTTCTTCAT 420
Db |||
QY 544 CTGAATCAGATTTAGTCTCCATCAATAAAGAGAGTCTCTTCAAAACAACTTCTTCAT 603
Db |||
QY 421 TCATCTCAGAGATGCTCCGAGATTTTGACAGCTCTCTGCTGACACTCTTTGTCCCAT 480
Db |||
QY 604 TCATCTCAGAGATGCTCCGAGATTTTGACAGCTCTCTGCTGACACTCTTTGTCCCAT 663
Db |||
QY 481 CTGTGTACACCGGAGTGTGTTAGTCAAGCTCCCACTAAACATCATGSCCATCGTTGTGT 540
Db |||
QY 664 CTGTGTACACCGGAGTGTGTTAGTCAAGCTCCCACTAAACATCATGSCCATCGTTGTGT 723
Db |||
QY 541 TCATCCTG 548
Db |||
QY 724 TCATCCTG 731

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RESULT 3

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US-10-208-408-24
; Sequence 24, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,868
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 3299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 2456481CBI
; US-10-208-408-24

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; FEATURE:
; NAME/KEY: allele
; LOCATION: (3996)..(3996)
; OTHER INFORMATION: PS7: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4624)..(4624)
; OTHER INFORMATION: PS8: polymorphic base guanine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4741)..(4741)
; OTHER INFORMATION: PS9: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4944)..(4944)
; OTHER INFORMATION: PS10: polymorphic base cytosine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (5024)..(5024)
; OTHER INFORMATION: PS11: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (5204)..(5204)
; OTHER INFORMATION: PS12: polymorphic base thymine or cytosine
US-10-176-464A-1

Query Match      55.0%; Score 301.6; DB 13; Length 6203;
Best Local Similarity 99.7%; Pred. No. 7.5e-82;
Matches 301; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 247 CAGATCAAAAGCACAAATGCCACTTAGATCCCGGTCAATTTCTTCTCAGGAACCCCA 306
DB 247 CAGATCAAAAGCACAAATGCCACTTAGATCCCGGTCAATTTCTTCTCAGGAACCCCA 4027
QY 307 ATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAACTGAAT 366
DB 4028 ATGATAAATATGAACCAATTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAACTGAAT 4087
QY 367 ACAGATTAGTCTCCATCAATAAAGCAGTCCCTTTCRAAACAACCTCCCTGCATTCATCT 426
DB 4088 ACAGATTAGTCTCCATCAATAAAGCAGTCCCTTTCRAAACAACCTCCCTGCATTCATCT 4147
QY 427 CAGAAGATGCTCCCGGATATTGACCACTCTCTGCTGACACTCTTTGTCCTCATCTGTGT 486
DB 4148 CAGAAGATGCTCCCGGATATTGACCACTCTCTGCTGACACTCTTTGTCCTCATCTGTGT 4207
QY 487 ACACCGGAGTGTGTTAGTCACTCCCACTAAACATCATGCCATCGTTGTGTTATCC 546
DB 4208 ACACCGGAGTGTGTTAGTCACTCCCACTAAACATCATGCCATCGTTGTGTTATCC 4267
QY 547 TG 548
DB 4268 TG 4269

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RESULT 6
US-09-918-995-16689
; Sequence 16689, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16689
; LENGTH: 405
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-918-995-16689

Query Match      43.1%; Score 236.2; DB 11; Length 405;
Best Local Similarity 91.6%; Pred. No. 2.6e-62;
Matches 272; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

QY 253 CAAAGCAACAATGCCACTTAGATCCCGGTCA-TTTTCTTCTCAGGAACCCCAATGAT 311
DB 1 CACAAGCAATAAATGCTATTTTAGAAGCGCGCATTTTTTCTCATTAACCGGAAGAT 60
QY 312 AAATATGAACCAATTTGGGAGGATGAGGAGAAAATGAAAGTGGGTAACTGAATACAGA 371
DB 61 AAATATGAACCAATGGGGGAGGATGAGGAGAAAATGAAAGTGGGTAACTGAATACAGA 120
QY 372 TTAGTCTCCATCAATAAAGAGCAGTCTCTTTCAAAAACAACCTCCCTGCATTCATCTCAGAA 431
DB 121 TTAGTCTCCATCAATAAAGAGCAGTCTCTTTCAAAAACAACCTCCCTGCATTCATCTCAGAA 180
QY 432 GATGCTCCGATATTTGACCGAGTCTCTGCTGACACTCTTTGTCCTCATCTGTGTACACC 491
DB 181 GATGCTCCGATATTTGACCGAGTCTCTGCTGACACTCTTTGTCCTCATCTGTGTACACC 239
QY 492 GGAGTCTTTGTAGTCACTCCCACTAAACATCATGCCATCGTTGTGTTATCTCCTG 548
DB 240 GGAGTCTTTGTAGTCACTCCCACTAAACATCATGCCATCGTTGTGTTATCTCCTG 296

RESULT 7
US-10-311-455-654/C
; Sequence 654, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 654
; LENGTH: 6436
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-654

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Query Match      27.0%; Score 148.2; DB 13; Length 6436;
Best Local Similarity 72.5%; Pred. No. 1.3e-34;
Matches 192; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 CGCGGAGGTCGCTTGGACCTGATCTTACCCGTGGGCGACCTGCGCTGCTGCTGCGCG 60
DB 1249 CGCGGAAAATCGCTTAAACCCCTTAATCTTACCCGTAAACACCCCTACGCTTACTACCGG 1190
QY 61 AAGACCGGCTCCCGGAGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 1189 AAAACCGACTCCCGGAGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1130
QY 121 GGGGCGAGCTCCCGGAGCGCGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCTGC 180
DB 1129 GAAACAACTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1070
QY 181 TGCTGGTGGCGGCTCTGCTTCACTGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

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; LOCATION: (901)..(960)
; OTHER INFORMATION: N's represent nucleotides between PS8 and PS9
; FEATURE:
; NAME/KEY: allele
; LOCATION: (990)..(990)
; OTHER INFORMATION: PS: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1021)..(1080)
; OTHER INFORMATION: N's represent nucleotides between PS9 and PS10
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1110)..(1110)
; OTHER INFORMATION: PS10: polymorphic base cytosine or guanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1141)..(1200)
; OTHER INFORMATION: N's represent nucleotides between PS10 and PS11
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1230)..(1230)
; OTHER INFORMATION: PS11: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)..(1320)
; OTHER INFORMATION: N's represent nucleotides between PS11 and PS12
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1350)..(1350)
; OTHER INFORMATION: PS12: polymorphic base thymine or cytosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1381)..(1440)
; OTHER INFORMATION: N's represent nucleotides 3' of PS12
US-10-176-464A-66

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Query Match      18.7%; Score 102.4; DB 13; Length 1440;
Best Local Similarity 38.3%; Pred. No. 7.9e-21;
Matches 141; Conservative 2; Mismatches 218; Indels 7; Gaps 1;

QY      1  CGCGAGGTCGCTGGACCTGATCTTACCGTGGGACCGCTGCGCTCTGCTGCGCG 60
Db      1  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
483  CGCGAGGTCGCTGGACCTGATCTTACCGTGGGACCGCTGCGCTCTGCTGCGCGNN 542

QY      61  AAGACCGGCTCCCGACCGCAGAGTCAGGTCAGGAGAGGTCGAGCGGAGCGCGGCG 120
Db      61  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
543  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 602

QY      121  GGGCAGGCTCCCGAGGAGCGCGCGGAGCGCGGAGCAATGGGGCGGCGGCTGC 180
Db      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603  CGGCTCCCGACCGCAGAGTCAGGAGAGAGGTCGAGCGGAGCGCGGAGGCG--- 658

QY      181  TGTGTGTGGCGCGCTGCTTACGTCTGTGCGCGCGCTGTGCTGCGCGACCGGCGCC 240
Db      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
659  ---GNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 715

QY      241  GCAGCGCAGATCAAGAGCAAAATGCCATTTAGATCCCGGTCATTTCTTCTCAGGA 300
Db      241  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
716  NNNNNNTCAGAAATCAAGAGCAAAATGCCATTTAGATCCCGGTCATTTCTTCTCAGGA 775

QY      301  ACCCCATGATAATATGACCATTTTGGAGGATGAGGAGAAAATGAAGTGGGTAA 360
Db      301  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
776  ACCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 835

QY      361  CTGAATAC 368
Db      361  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
836  NNNNNNTCC 843

RESULT 10
US-09-925-664-33
; Sequence 33, Application us/09925664
; Patent No. US2002016006A1

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; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENITOPE-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(189)
; OTHER INFORMATION:
US-09-925-664-33

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Query Match      8.1%; Score 44.6; DB 10; Length 192;
Best Local Similarity 71.1%; Pred. No. 0.0018;
Matches 59; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      273  TTGATCCCCGCTCATTTCTCTCAGGAACCCCAATGATGAATATGAACCATTTTGGGAG 332
Db      273  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1  TTGATCCACGATCGTTTCTATTGCGCAATCCAAATGATAGTACGAACCATTTTGGGAA 60

QY      333  GATCAGGAGAAAAATGAAAGTGG 355
Db      333  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61  GATCAGCAAGATGCTGAGTGG 83

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RESULT 11
US-10-029-386-24941
; Sequence 24941, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24941
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002504.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: NT HIT: AY038071.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A1656304.1, EVALUE 2.00e-42
; OTHER INFORMATION: SWISSPROT HIT: O35085, EVALUE 7.00e-64
US-10-029-386-24941

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Query Match      8.1%; Score 44.4; DB 13; Length 897;
Best Local Similarity 59.7%; Pred. No. 0.0045;
Matches 92; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY      38  CACCTTGGCTCTGCTGCGGAGAACCGGCTCCCGACCGCAGAGTCAAGTCAAGAGAGAG 97
Db      38  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300  CAGCCGCGAGCAAGTCGTACCGCGAGAACGGGGCGCCCTTCTGTCGCCGCCGCCGCT 359

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QY 98 GGTGAAGCGGAGCAGCCCGAGCGCGCAGCCTCCCGGAGCAGCGCCGCGCAGAGCCCGG 157
Db 204 GGTGAGGCGCGCAGACAGCGTAGCGAGGGCTTGAGCGCGCGCGCACCGGTGGCGCCGC 145
QY 158 GACAAATGGGCGCGCGCGCTGCTGCTGTGTGCGCGCCTGCTTCACTCTGTGTGGCGCCGCT 217
Db 144 GACGGGGCGGTGTTCCGACCGGCTCCCGCGCGGCTCGTCGGCGGTGAGCAGCGCGGC 85
QY 218 GTTGTCTGCCCGCACC CGCGCGCGCAGCGCAGATCAAAAGCAAAATGCC 269
Db 84 CGTGCTCGCGCGCGCGCGCGCCAGGACAGCGGCACCGCGGAGCAACGCC 33
```

RESULT 15

```
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

```
Query Match 7.7%; Score 42.4; DB 15; Length 9025608;
Best Local Similarity 52.9%; Pred. No. 1.9;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 98 GGTGAAGCGGAGCAGCCCGAGCGCGCAGCCTCCCGGAGCAGCGCCGCGCAGAGCCCGG 157
Db 8703823 GGTGAGGGCGCGCAGACAGCGTAGCGAGGGCTTGAGCGCGCGGCACCGGTGGCGCCGC 8703764

QY 158 GACAAATGGGCGCGCGCGCTGCTGCTGTGTGCGCGCCTGCTTCACTCTGTGTGGCGCCGCT 217
Db 8703763 GACGGGGCGGTGTTCCGACCGGCTCCCGCGCGGCTCGTCGGCGGTGAGCAGCGCGGC 8703704

QY 218 GTTGTCTGCCCGCACC CGCGCGCGCAGCGCAGATCAAAAGCAAAATGCC 269
Db 8703703 CGTGCTCGCGCGCGCGCGCGCCAGGACAGCGGCACCGCGGAGCAACGCC 8703652
```

Search completed: December 20, 2003, 23:30:48
Job time : 272 secs